

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:36:09 ; Search time 42 Seconds

(without alignments)

1184.383 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSSRTKTESQQSQQGTTSSSS.....ASTSSCSEILPTSAEKRKAR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	621	22.9	513 1 S43941	protein kinase DUN1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
2	593.5	21.9	374 1 S5193	N;Alternate names: Protein D370; protein YDL10ic
3	591.5	21.8	370 1 S57347	C;Species: Saccharomyces cerevisiae
4	575.5	21.2	821 1 A39616	C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
5	563.5	20.8	460 2 S58882	C;Accession: S43941;
6	560.5	20.7	301 1 A40811	A;Title: DUN1 encodes a protein kinase that controls the DNA damage response in yeast.
7	539.5	19.9	469 1 S1656	A;Reference number: S43941; PMID:3261511
8	538	19.8	445 2 T4420	A;Accession: S43941;
9	537	19.8	348 2 T37321	A;Molecule type: DNA
10	535	19.7	524 2 A45472	A;Residues: 1-513 <BAL>
11	534.5	19.7	474 1 T9TC4	A;Cross-references: EMBL:274149; NID:91431139; PID:91431140; GSPPDB:GN0001
12	534.5	19.7	502 2 I5637	A;Experiment source: strain S288C
13	531	19.6	473 1 A51036	R;Boskovic, J.; Saiz, J. B.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Ballesta, J. P. G.; Remacha, M.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Zhou, Z.; Elledge, S.J.; Cell 75, 1119-1127, 1993.
14	507.5	18.7	735 2 S5330	A;Reference number: S67639
15	506	18.7	560 2 S51600	A;Accession: S67643
16	503.5	18.6	735 2 I51901	A;Molecule type: DNA
17	501.5	18.5	414 2 JN0323	A;Residues: 1-513 <SAI>
18	501.5	18.5	504 2 T10449	A;Cross-references: EMBL:X5644; NID:91199535; PID:CAA64912.1; PID:91199548
19	501	18.5	512 1 JC1446	A;Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevi
20	498	18.4	724 1 B3571	A;Accession: S72106
21	498	18.4	608 2 T18445	A;Accession: S72106
22	494.5	18.2	516 1 JU0270	A;Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevi
23	493.5	18.2	509 2 B4412	A;Accession: S72106
24	493.5	18.2	530 2 D44112	C;Superfamily: protein kinase DUN1; kinase interaction domain homology; protein kinase hc
25	492.5	18.2	473 1 S59941	C;Keywords: Arp; nucleus; phosphoprotein; phosphotransferase; serine/threonine-specific I
26	490	18.1	511 1 A56109	F;58-128/Domain: kinase interaction domain homology <KIH>
27	488	18.0	512 2 T52633	F;198-480/Domain: protein kinase homology <KIN>
28	487	18.0	504 2 T39226	F;206-214/Region: protein kinase ATP-binding motif
29	484.5	17.9	542 2 T08777	F;206-214/Region: protein kinase ATP-binding motif

RESULT 1

S43941

protein kinase DUN1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)

N;Alternate names: Protein D370; protein YDL10ic

C;Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S43941;

R;Zhou, Z.; Elledge, S.J.

Cel1 75, 1119-1127, 1993.

A;Title: DUN1 encodes a protein kinase that controls the DNA damage response in yeast.

A;Reference number: S43941; PMID:94084787; PMID:3261511

A;Accession: S43941

A;Molecule type: DNA

A;Residues: 1-513 <BAL>

A;Cross-references: EMBL:274149; NID:91431139; PID:91431140; GSPPDB:GN0001

A;Experiment source: strain S288C

R;Boskovic, J.; Saiz, J. B.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Ballesta, J. P. G.; Remacha, M.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Zhou, Z.; Elledge, S.J.; Cell 75, 1119-1127, 1993.

A;Reference number: S67639

A;Accession: S67643

A;Molecule type: DNA

A;Residues: 1-513 <BAL>

A;Cross-references: EMBL:274149; NID:91431139; PID:91431140; GSPPDB:GN0001

A;Experiment source: strain S288C

R;Boskovic, J.; Saiz, J. B.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Ballesta, J. P. G.; Remacha, M.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Zhou, Z.; Elledge, S.J.; Cell 75, 1119-1127, 1993.

A;Reference number: S67639

A;Accession: S67643

A;Molecule type: DNA

A;Residues: 1-513 <BAL>

A;Cross-references: EMBL:274149; NID:91431139; PID:91431140; GSPPDB:GN0001

A;Experiment source: strain S288C

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A;Reference number: S67639

A;Accession: S67643

A;Molecule type: DNA

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A;Reference number: S67639

A;Accession: S67643

A;Molecule type: DNA

A;Residues: 1-513 <BAL>

A;Cross-references: EMBL:274149; NID:91431139; PID:91431140; GSPPDB:GN0001

A;Experiment source: strain S288C

R;Boskovic, J.; Saiz, J. B.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Ballesta, J. P. G.; Remacha, M.; Soler-Mira, A.; Garcia-Cantalejo, J. L.; Revuelta, J. L.; Jiminez, R;Zhou, Z.; Elledge, S.J.; Cell 75, 1119-1127, 1993.

A;Reference number: S67639

A;Accession: S67643

A;Molecule type: DNA

A;Map position: 4L

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine

Ca2+/calmodulin-dependent

Query Match Similarity 22.9%; Score 621; DB 1; Length 513;
 Best Local Similarity 32.1%; Pred. No. 2.2e-21; Gaps 12;
 Matches 149; Conservative 73; Mismatches 152; Indels 90; Gaps 12;

Qy 88 GRDKKCDYTFDIPVNLQDTRYKTSRKRFRIFQELGRGHRSRVAVIDLSNGTFVNKEIT 147
 Db 59 GRSRSCDV----ILSPED-1STPHAEFHLLQMDVNFQRNLINVTDKSNQTFNGNRL 112
 Qy 148 GKRTLPLTNNAEIALSLPTNKFVFV----SDLSDVDDQT 183
 Db 113 VK-KDYLKINGDRIVFGKSCSLFKYASSSSTDIEENDDEVSSRSYKNDDEVFKKPQI 171
 Qy 184 -----YKDFDLKYMNSRPISSGACCEVKAQFKSQVCKKVAYKII 223
 Db 172 SATSSONATSSAIAIRKLNKTRVSEFVKYLUKGKELGAGHAYLKVKPAKNTGQAVKF 231
 Qy 224 SKR---FKAQTSSNEHPISVDTIEILKQDHDPCITK----IENFEDSDDFYIVL 275
 Db 232 HAQQNDQDKKQKFRE----ETNLMRQHNPVNVLDSFVEBISKQIQYLVLEK 284
 Qy 276 MEGGELFDVYNSTRLEPPIAKLYFYOMLALAYQYLHENGYTHRDLPKPNVLLSTSEE-- 333
 Db 285 IDGELPERVTKTCURQDEVALKFQKLLGKLYLBNQI1THRDLPKPNVLLTRRNPF 344
 Qy 334 -----CC1K1TDFGOSKTLGTSLSMRTLUGCTPTYLAPENVNTAGTGYSSA 379
 Db 345 SOYQLGPWDEDEIDIOVKIADEGLAKPTGEMOFTNLCGPSVYAPEVLT--KKGYTSK 401
 Qy 380 VDCWSLGVILTVCLGCPPFSEQNSNIPLNKQIAEGKTYTAIAAMRNVSSEAFDLVNL 439
 Db 402 VDLWSAGVILVCLGCPPFSDQLGPPSLKEQILQKARYFAFSPYNDKIDDSVLHLISNL 461
 Qy 440 VVDPEQRLLTQKALEHFWLQD---DSMKHTVERLNYGVDTHTMP 479
 Db 462 VLNPDERYNIDEALNHWFWNDIQQQSSVSLELQRLQI-TDNKIP 504

RESULT 2

S50193

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat

N: Alternative names: CAMKII

C: Species: Homo sapiens (man)

C: Date: 10-Sep-1999 #Sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C: Accession: S57347

R; Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, B.G.; Tomhave, E.D.; Edelman, A.M.; Cho, F.S.; Phillips, K.S.; Bogucki, B.I.; Weaver, T.E.

A; Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struct

A; Reference number: S57347; MUID:25369239; PMID:7641687

A; Accession: S57347

A; Status: Preliminary; nucleic acid sequence not shown

A; Cross-references: UNIPROT:Q14012; EMBL:L41816; NID:9790789; PID:9790789

C: Genetics: A; Gene: GNB:CAMKII

A; Cross-references: GDB:642249

C: Keywords: Ca2+calmodulin-dependent protein kinase I; protein kinase; homology

C: Status: Preliminary; protein kinase; phosphoprotein; phosphotransfer

A; Molecule type: mRNA

R; Picciotto, M.R.; Cernik, A.J.; Nairn, A.C.

J. Biol. Chem. 268, 26512-26522, 1993

A; Reference number: S50193; MUID:95035115; PMID:7948038

A; Status: preliminary

A; Molecule type: mRNA

A; Accession: A49682

A; Status: preliminary

A; Molecule type: mRNA

R; Mochizuki, H.; Ito, T.; Hidaka, H.

J. Biol. Chem. 268, 9143-9147, 1993

A; Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase V

A; Reference number: A46038; MUID:8386178

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-374 <C>

A; Cross-references: UNIPROT:Q63450; EMBL:L26288; NID:94396

A; Status: preliminary

A; Molecule type: protein

A; Accession: A46038

A; Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HOPG', '327, 'T', 329, 'TDS' <P>;

A; Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase I;

A; Reference number: A46038; MUID:93232082; PMID:8386178

A; Status: sequence extracted from NCBI backbone (NCBIP:129927)

C; Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology

C; Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer; F; 18-276/Domain: protein kinase homology <KIN> F; 26-34/Region: protein kinase Arp-binding motif F; 302-314/Region: calmodulin binding F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 21.9%; Score 593.5; DB 1; Length 374;

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 21.9%; Score 593.5; Pred. No. 2.9e-20; Gaps 5;

Best Local Similarity 39.9%; Mismatches 106; Indels 19; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 186 KDFIDKYMMSRPISSGACCEVKAQFKSQVCKKVAKIIAKCKAEGKSMEN----EI 245

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 186 KDFIDKYMMSRPISSGACCEVKAQFKSQVCKKVAKIIAKCKAEGKSMEN----EI 67

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 186 KDFIDKYMMSRPISSGACCEVKAQFKSQVCKKVAKIIAKCKAEGKSMEN----EI 67

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 186 KDFIDKYMMSRPISSGACCEVKAQFKSQVCKKVAKIIAKCKAEGKSMEN----EI 67

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match Similarity 186 KDFIDKYMMSRPISSGACCEVKAQFKSQVCKKVAKIIAKCKAEGKSMEN----EI 67

Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

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Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

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Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

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Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

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Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

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Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

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Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

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Best Local Similarity 39.9%; Pred. No. 2.9e-20; Gaps 5;

Matches 124; Conservative 62; Mismatches 106; Indels 19; Gaps 5;

F; 177/Binding site:

Db	68	AVLHKIKPHNIVADLIVYSESCHGHLIMOLVSGGELDVRIVKGFYTERDASRLIFQVL	D	127	Best Local Similarity 28.6%; Pred. No. 4e-19; Matches 148; Conservative 81; Mismatches 166; Indels 123; Gaps 12;
Qy	306	AVQYLHENGIVHDLKPENVLVLSSTSECCIKITDFEQSKLGETSMRITLGTPYIAP	365	63	Qy 10 SQOSQPTSSSSAAQSYSSSSSS----GTLSSPDTPVQDL-ASIPDEPEIDBDIPQ
Db	128	AVKYLHDLGIVHDLKPENLIVYLSLDESDKIMISDFGSLKMEPDGSVLSLACCTGPGVAP	187	64	Db 5 TQPTQSTQATQFRL1BKFSDQIGENIVCRVICITGQIPTRDLSADISQVLEREKESIKK
Qy	366	EVLTNTAGTTGYSVAVDCWMSLGTVLFVUCIGYPFPSEONSTPLKNOIAEGKTYTIAAMR	425	64	Qy 64 PWGRILWALGKGFLNHCLHEBYVFGDKKCDYTDFDPLVLAQTDRTYTSKRHFRIFQELG
Db	168	EVL--AOKPYSKAVDCWMSLGTVLFVUCIGYPFPYDN--DARLFEQILKAETFDFSPYWD	243	123	Db 65 Vw-----TFRGNPACY-----HLGNI3RLSNKHFQIIL--LG
Qy	426	NYSEQAQFDLVKNUVVDPBQLRITTKOALEHPNQLDSSMKHTVERLAVGVDHTMPPPIKKN	485	94	Qy 124 HGHSRVANIEDLSGNGTSPVNUKEIIGKRTPLTNNAEI-----
Db	244	DISDAKDFRHMKEDEPKRTFCEQALQHPWTAQDT----ALDKNIHQSVSEQIKNN	297	161	Db 95 EDGNLILN-DISTNCTWLNSQKVBNSNQLSOGGBITVGVGEVDLSLIVFINDKFK
Qy	486	IIRKRGHHDWQ 496	505	152	Qy 162 -----ALSLPNKRVFESDLVDDQTYPKDFIDK
Db	298	FAKSKE--WRQ 305	505	191	Db 153 QCLEQNQKVDR1RSNLKNTSKIASPGITSSTASMSYMNKTGFKDFSTIDEV-----
Qy	505	YIMSRPIGSGAGCEVFLAFQSVCKRVAKLISKRKFRKMTSSNEHPIVSUDETEIELKLKL	521	203	Qy 192 YIMSRPIGSGAGCEVFLAFQSVCKRVAKLISKRKFRKMTSSNEHPIVSUDETEIELKLKL
Db	505	Db 204 -----VGQGAFATVKRAIERTTGFCAVLLISQRKVIGNM-----GIVTRELETQKL	521	251	Db 204 -----VGQGAFATVKRAIERTTGFCAVLLISQRKVIGNM-----GIVTRELETQKL
Qy	521	A39616 (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)	521	311	Qy 252 DHPC1K1ENFDSEDFYYVYLEMGGELDRVNISTRLEPIAKLYFQMLLAVQYLH
C;Species		Saccharomyces cerevisiae	521	311	C;Species: Schizosaccharomyces pombe
C;Date		20-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004	521	311	C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession		A39616; S6516; S6516; S69446; S13321	521	311	C;Accession: S58882
R;Stern, D.P.; Zheng, P.; Beiderl, D.R.; Zerillo, C.		Mol. Cell. Biol. 11, 987-1001, 1991	371	311	R;Murakami, H.; Okayama, H.
A;Title		A;Title: Spk1, a new kinase from Saccharomyces cerevisiae, phosphorylates proteins on serine/threonine residues.	370	370	A;Title: A kinase from fission yeast responsible for blocking mitosis in S phase.
A;Reference number		A;Reference number: A39616; MUID:9117267; PMID:1899289	370	370	A;Reference number: S58882; MUID:95240713; PMID:7723827
A;Accession		A;Accession: A39616	370	370	A;Accession: S58882
A;Molecule type		A;Molecule type: DNA	370	370	A;Molecule type: mRNA
A;Residues		A;Residues: 1-821 <STB>	370	370	A;Residues: 1-60 <MUR1>
A;Cross-references		A;Cross-references: UNIPROT:P22216; GB:MM5623; PIDN:AAA35070_1; PMID:g172657	370	370	A;Cross-references: S71846
A;Experimental source		A;Experimental source: strain S288C	370	370	A;Experimental source: mRNA
A;Purnelle, B.; Coster, F.; Goffeau, A.		A;Purnelle, B.; Coster, F.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.P.	370	370	A;Purnelle, B.; Coster, F.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.P.
A;Reference number		A;Reference number: S65154	370	370	A;Reference number: S71846
A;Accession		A;Accession: S65164	370	370	A;Accession: S71846
A;Molecule type		A;Molecule type: DNA	370	370	A;Molecule type: mRNA
A;Residues		A;Residues: 1-821 <PUR>	370	370	A;Residues: 1-60 <PUR2>
A;Cross-references		A;Cross-references: EMBL:273509; NID:g1370325; PID:CAA97858_1; PMID:g1370326; GSPDB:GN00	370	370	A;Cross-references: EMBL:X85040; NID:g794146; PMID:CAA59410_1; PMID:g794147
A;Experimental source		A;Experimental source: strain S288C (AB972)	370	370	A;Cross-references: T41204
R;Purnelle, B.; Combliz, S.; Coster, F.; Goffeau, A.		R;Purnelle, B.; Combliz, S.; Coster, F.; Goffeau, A.	370	370	R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
A;Description		A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identities	370	370	A;Description: submitted to the EMBL Data Library, March 1996
A;Reference number		A;Reference number: S69428	370	370	A;Reference number: S71846
A;Accession		A;Accession: S69428	370	370	A;Accession: S71846
A;Molecule type		A;Molecule type: DNA	370	370	A;Molecule type: DNA
A;Residues		A;Residues: 1-821 <PUR>	370	370	A;Residues: 1-202, 'F', 204-237, 'F', 239-460 <NOO>
C;Genetics		C;Genetics: SGD:RAD53; SPK1; MEC2; SAD1; MIPS:YPL153C	370	370	C;Cross-references: EMBL:1070376; NID:9501965; PIDN:CA5B2158_1; PID:95701966; GSPDB:GN00
A;Cross-references		A;Cross-references: SGD:S0006074; MIPS:YPL153C	370	370	A;Cross-references: R;Lindsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Murray, J.M.; Christensen, P.U.; Murray, J.M.; Osmar
A;Map position		A;Map position: 16L	370	370	A;Map position: 16L
C;Function		C;Function: serine/threonine-specific protein kinase	370	370	C;Function: submitted to the EMBL Data Library, July 1999
A;Note		A;Note: contains low activity as tyrosine-specific protein kinase	370	370	A;Note: contains low activity as tyrosine-specific protein kinase
C;Superfamily		C;Superfamily: protein kinase SPK1; kinase interactin domain homology; protein kinase h	370	370	C;Superfamily: protein kinase SPK1; kinase interactin domain homology; protein kinase h
F;68-133/Domain		F;68-133/Domain: kinase interaction domain homology <KIH>	370	370	F;68-133/Domain: kinase interaction domain homology <KIH>
F;196-466/Domain		F;196-466/Domain: protein kinase homology <KIN>	370	370	F;196-466/Domain: protein kinase homology <KIN>
F;204-113/Region		F;204-113/Region: protein kinase ATP-binding motif	370	370	F;204-113/Region: protein kinase ATP-binding motif
F;227/Active site		F;227/Active site: Lys #status predicted	370	370	F;227/Active site: Lys #status predicted
Query Match		21.2% Score 575.5 DB 1; Length 821;	370	370	Query Match

A;Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint
 A;Reference number: 226084; MUID:98119835; PMID:9450932
 A;Accession: T52473
 A;Molecule type: DNA
 A;Residues: 1-205; 'I', 204-237, 'F', 239-460 <LIN>
 A;Cross-references: EMBL:AU222869; NID:92689196; PIDN:CAA11019.1; PID:92689197
 C;Genetics:
 A;Gene: SPBC18B5.1.1c; cds1
 A;Map position: 3
 A;Intzone: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
 C;Function:
 A;Description: EC 2.7.11.- protein kinase Cds1 [validated, MUID:98119835]; is required to
 A;Note: not activated by S-phase arrest and activated by DNA damage
 A;Superfamily: protein kinase Cds1; kinase interaction domain homology; Protein kinase C
 C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F;6-265/Domain: protein kinase homology <KIN>
 F;14-22/Region: protein kinase ATP-binding motif
 F;165-433/Domain: kinase interaction domain homology <KIN>
 F;173-181/Region: protein kinase ATP-binding motif

Query Match Score 563.5; DB 2; Length 460;
 Best Local Similarity 33.3%; Pred. No. 7.8e-19;
 Matches 14/4; Conservative 75; Mismatches 163; Indels 51; Gaps 13;

Qy 87	FRGRDKKCDTTEFDLPIVNLQTDRTKTYSKRHFRTFQELGHGH----SRVANTEDLISGNGT	F 141	Db 62	FRGRHKSCSCEVNLQG-----RVSNEHFTEYQ-----GRHNRSDDESNVVFHDHSNGT	F 110
Qy 142	VNKEIIGKGRTRPLTNNAE--IALSPLPTNKFVFSDSL-----DDOTIYKDFDQYIMS	195	Db 111	LNFERLAKNSRTRLNSDEIRGLGVPKDEISFLQCVPKHSRDSQKNMKSENHYELI	170
Qy 196	RPIGSAGCEVKAQSKVCKKAVKLIISKRKFKONTSNNEHNPISVDTIEBLKLDHPC	255	Db 171	RTLGSCTPAAVVKLAVENNSGKRYAIKINRKKLTSSEKRATENFQREDILKSLHHPG	230
Qy 256	IIKIENFDFDSEFYITLMEGGELFDRYVNSTRLEPATAKLYFQMLLAVQVHLHENGV	315	Db 231	VVQCHEFOENDDEFLVMEYYEGGDLMDFLNLANGSDEQDCKPLKQLLTLTHHKQGY	290
Qy 316	IHRDLKDENVLSSTSSECCIKITDFGQSKL-GETSLMRTLICGTPYLAPEVINTAGT	374	Db 291	THRDIKPENLITN---DFHLKISDFGLAKVTHGTCFLFECGTMGYLAPEVLKSKNNV	347
Qy 375	--GYSPPAVDCMSLGVILLFVCLGYPFP--SQQNSNIPLKNQIAE8KTYTAAARVNVE	429	Db 348	LDGGYDDKDVMSLGCVLYMLTASPFASSQQAKCIEL--ISKGAYAPEPLNEISE	404
Qy 430	QAFDLVNLQLYVVDPEORLTQKALEHFWLQDDSMKHTVERMLYGDHTMPPPIKKNITRK	489	Db 405	EGIDLINRMLINPERKISSESSALQHWF-----YTVST----HEHRTPSSSE-----	449
Qy 490	RGEHWDQDASTSS 502		Db 450	-HEATEQLNSSS 460	

RESULT 6
 A40811 QAFDLVNLQLYVVDPEORLTQKALEHFWLQDDSMKHTVERMLYGDHTMPPPIKKNITRK 489
 A;Title: Dictyostelium discoideum
 A;Cross-references: UNIPROT: P08414; EMBL: X58995; NID: 950366; PIDN: CAA41741.1; PID: 950367
 R;Sikela, J.M.; Hahn, W.E.
 C;Species: Dictyostelium discoideum
 C;Date: 10-Apr-1992 #Sequence_change 21-Jan-1997 #text_change 09-Jul-2004
 R;Tan, J.L.; Spudich, J.A.
 J. Biol. Chem. 266, 16044-16049, 1991
 A;Reference number: A40811; MUID:91340753; PMID:1651931
 A;Accession: A40811
 A;Molecule type: mRNA
 A;Residues: 1-301 <TAN>
 A;Cross-references: UNIPROT: P25323; GB: M64176; NID: g200360; PIDN: AAA39933.1; PMID: g387512
 R;Tan, J.L.; Spudich, J.A.
 Genomics 4, 21-27, 1989
 A;Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
 A;Reference number: 149571; MUID: 89122027; PMID: 2536634
 A;Accession: I49571

J. Biol. Chem. 265, 13818-13824, 1990
 A;Title: Dictyostelium myosin light chain kinase. Purification and characterization.
 A;Reference number: A37125; MUID:9033797; PMID:2380188
 A;Accession: A37125
 A;Molecule type: protein
 A;Residues: 9-12, 'I', 14-19; 163-167, 'S', 169-179; 192-198 <TA2>
 C;Genetic ID:
 A;Gene: mlka
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine in itself
 A;Pathway: cytokinesis; fruiting body formation
 A;Note: not activated by Ca2+/calmodulin in contrast with MLCK from higher eukaryotes
 C;Superfamily: kinase-related transforming protein; protein kinase homology
 C;Keywords: ATP; autophosphorylation; cell division; phosphoprotein; phosphoprotein; phosphotransferase; P-6-265/Domain: protein kinase homology
 F;6-265/Domain: protein kinase homology <KIN>
 F;14-22/Region: protein kinase ATP-binding motif
 F;267-295/Domain: inhibitory #status predicted <INH>
 F;37/Active site: Lys #status predicted
 F;296/Binding site: phosphate (thr) (covalent) (by autophosphorylation) #status predicted
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine in itself
 A;Pathway: cytokinesis; fruiting body formation
 A;Note: not activated by Ca2+/calmodulin in contrast with MLCK from higher eukaryotes
 C;Superfamily: kinase-related transforming protein; protein kinase homology
 C;Keywords: ATP; autophosphorylation; cell division; phosphoprotein; phosphoprotein; phosphotransferase; P-6-265/Domain: protein kinase homology <KIN>
 F;6-265/Domain: protein kinase homology <KIN>
 F;14-22/Region: protein kinase ATP-binding motif
 F;267-295/Domain: inhibitory #status predicted <INH>
 F;37/Active site: Lys #status predicted
 Query Match Score 560.5; DB 1; Length 301;
 Best Local Similarity 38.7%; Pred. No. 7.1e-19;
 Matches 116; Conservative 58; Mismatches 105; Indels 21; Gaps 5;
 Query 192 YIMSRPIGSACGEVKAQVAKLISKRKFRNTSSNHPIVSVDTEBLKRL 251
 Db 8 YEFKEELGRGAFSIVYLGKQMLQYQMLLAVQYLN ---LKMEDVILKRY 62
 Query 252 DHPCITKIEFFDSEDFYYTIVELMEGGELFDRYVNSTRLEPATAKLYFQMLLAVQYLN 311
 Db 63 NHPNTIALKELFDTPERKLYLVMELVGGELFDK1LVEKGSYSEADANLYRKIVSAVGYLN 122
 Query 312 ENGVTHRDLKPEPVNLSSSECCIKITDFGOSKILGETSLMRTLICGTPYLAPEVINTA 371
 Db 123 GLNITYHDLKPEPNLILKSKENHLEAFGLSKLIGOTLAMQACTGTSYVAPENVLN -- 180
 Query 372 GTGTYSSAIDCWSLGVLFVCLGYPFPSEQNSNIP-LKNQIAQGKTYTAAARVNVSQ 430
 Db 181 -ATGYDKEVDMWSIGVITYLLCSPFPF--YGDVTPPEIPEQIMVNYPEEYNGGKSE 237
 Query 431 AFDLVYKNLIVVDPEORLTQKALEHFWLQDDSMKHTVERMLYGDHTMPPPIKKNITRK 490
 Db 238 AKDPIGKLIVVDVSKRLNATNALNHPWLKNSNSNNTIDV-----KMRKVYIVER 287
 A;Molecule type: mRNA
 A;Accession: S17656
 A;Cross-references: UNIPROT: P08414; EMBL: X58995; NID: 950366; PIDN: CAA41741.1; PID: 950367
 R;Sikela, J.M.; Hahn, W.E.
 C;Species: Mus musculus (house mouse)
 C;Sequence: S17656; 10-Sep-1999 #sequence change 09-Jul-2004
 C;Accession: S17656; A29878; T49571
 R;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
 FEBS Lett. 289, 105-109, 1991
 A;Title: cDNA sequence and differential expression of the mouse Ca (2+)/calmodulin-dependent
 A;Reference number: S17656; MUID: 91372388; PMID: 1893397
 A;Accession: S17656
 A;Molecule type: mRNA
 A;Residues: 1-469 <JON>
 A;Cross-references: UNIPROT: P08414; EMBL: X58995; NID: 950366; PIDN: CAA41741.1; PID: 950367
 R;Sikela, J.M.; Hahn, W.E.
 C;Species: Dictyostelium discoideum
 C;Date: 10-Apr-1992 #Sequence_change 21-Jan-1997 #text_change 09-Jul-2004
 R;Tan, J.L.; Spudich, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
 A;Title: Screening an expression library with a ligand probe: isolation and sequence of a
 A;Accession: A29878; MUID: 87204263; PMID: 3033675
 A;Molecule type: mRNA
 A;Residues: 315-469 <SIK>
 A;Cross-references: UNIPROT: P08414; EMBL: X58995; NID: 950366; PIDN: CAA41741.1; PID: 950367
 R;Sikela, J.M.; Hahn, W.E.; Spudich, J.A.
 Genomics 4, 21-27, 1989
 A;Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
 A;Reference number: 149571; MUID: 89122027; PMID: 2536634
 A;Accession: I49571

Qy	429	EQAFDLYKNNLIVVDPBOPBLTTKQALEHPWLQDDDSMKTHTVERLGYDHTMPPPIKNNIIR	488	277 K-KVEKGKYYFDFNDWKNIISBEAKBLIKLMLTYDYNKRITAKEALNSKWK 326
Db	249	GSAKDFITHMCCDPEARPTCQDALSHPWSGNT-----AYTHDIHGTVAHLKSLAK	302	RESULT 11
Qy	489	K 489		
Db	303	R 303		
RESULT 10				
A45472				
protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)				
protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)				
C;Species: Plasmodium falciparum				
C;Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 09-Jul-2004				
C;Accession: A45472; E71605; S28590				
R;Zhao, Y.; Kappes, B.; Franklin, R. M.				
J. Biol. Chem. 268: 4347-4354, 1993.				
A;Title: Gene structure and expression of an unusual protein kinase from Plasmodium falciparum				
A;Reference number: A45472; MUID:93179444; PMID:8440720				
A;Contents: K1				
A;Accession: A45472				
A;Molecule type: DNA				
A;Residues: 1-524 <ZHA>				
A;Cross-references: UNIPROT:Q27731; EMBL:X67288; NID:98877; PID:CAA7704_1; PMID:99878				
A;Note: sequence extracted from NCBI backbone (NCBIN:125849, NCBI:125850);				
R;Gardner, M.J.; Tettelin, H.; Cuccia, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Partea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 28(1):1126-1132, 1998				
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.				
A;Reference number: A71600; MUID:99021743; PMID:9804551				
A;Accession: E71605				
A;Status: nucleic acid sequence not shown; translation not shown				
A;Molecule type: DNA				
A;Residues: 1-524 <GAR>				
A;Cross-references: GB:AE001419; PID:93845281; PIDN: AAC71952_1; PMID:g384528				
A;Experimental source: clone 3D7				
C;Genetics:				
A;Gene: cpk; PF00815W				
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase F; 62-70/Region: protein kinase ATP-binding motif				
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific F; 54-325/Domain: protein kinase homology <KINs>				
F;416-448/Domain: calmodulin repeat homology <EP4>				
Query Match Score 19.78; Best Local Similarity 35.3%; Pred. No. 1.7e-17; Matches 124; Conservative 60; Mismatches 125; Indels 42; Gaps 7;				
Qy	125	GHSRVANTEDSLGSNQGTFVNKEITIGKRTLPTNNAAITALSLPTPNKTVFVFSPLSDVQDITY 184		
Db	2	GSQSSNVRDF-----KTRSKFTGNGNYGKGSNNK-----NSBDAIN 40		
Qy	185	PKDFIDK-----YIMSRPIGSGAGCEVKAQFKSVCKVAVKIKSKFKANTISSNE 236		
Db	41	PSMYVRKEKGKIGESEYPKVKGSGAYEVILCREKGHGGEKAIKVKKQFDKMKYKST 100		
Qy	237	HPISVD-----TEFBILKLDHPCLIKENFOSEDFYVYVDELMEGELFGRVNS 288		
Db	101	NKIECDDKHKHETEYNEISLKLSDHNPITKLFDVFDKKYFVLYTEFYEGELFQIINR 160		
Qy	289	TRLREPIAKTYYQMLIAVQYHENGTHRDIKPENYLSTTSEBCKTDFGOSKILG 348		
Db	161	HKFDCECDANIMKQIISGICLKHKNIVHRDKPENILLENKHSUNIKVDFGJSSFFS 220		
Qy	349	ETSLMRTLUGPTPTYLAEVBLVNTAGTAGTGYSAVDCMISGLVLFVCLGYPPESEQNSNIP 408		
Db	221	KDNKLRDRLGATYAYIABVLRK-----YNBECDDVWVSCGVVILYLLGYPFGQNDQDII 276		
Qy	409	KNQIAEGKTYIAAWNVEQAFDLYKNNLUVDPPEORLTQKQALPHPWLQ 459		

C;Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/threonine kinase; domain: protein kinase homology <KIN>
 P;40-296/Domain: protein kinase homology <KIN>
 P;4-8-57/Region: protein kinase ATP-binding motif
 F;318-337/Region: calmodulin binding #status predicted <CSB>
 F;71/Active site: Lys #status predicted

Query Match 12
 Best Local Similarity 39.8%; Score 534.5; DB 1; Length 474;
 Matches 117; Conservative 52; Mismatches 104; Indels 21; Gaps 3;

Qy 174 SDSLVDQDQTPYKDPDKK-----YIMSRPIGSAGEYKLAFOKSVCVKVAKIIS 224
 Db 15 SSVSSTSNEHPIVDPSKRDPLSDFPEVESELGRGATSYVRCKQKGTKQYALKVLY 74
 Qy 225 KRFKFKNTSNEHPIVSVDTEILKQKDPDKCIIENPDSDFYYVTEILMEGGELFDR 284
 Db 75 KTVDDKK-----IVRTETGIVLRLSHPNIIKLEIETPEISLVLVLTGGELFDR 125
 Qy 285 VNSTRTRREPPIAKLYFYQMLLAQYIHLGNGVTHRLDPKENVILSSTSSECCIIKTDGQS 344
 Db 126 IVEKGYYSSRDAADAVQKQLEAYLHENGIVRDLRPNLYATPAPDAPKIAIDGLS 185
 Qy 345 KILGETSLMRLTLCGTPYIAPAEVINTAGTCGSSAADCWLSGVILFVLCGYPFPSEQNS 404
 Db 186 KTEHQVNLMTKTVCTPGCPTLRGQ--AVGPEVDMWSVGLTGYIILCPFPYDVRG 242
 Qy 405 NIPLKQNLQAGKTYIAAWRNVSEQADLVRKNLVVDPEQRLTQKALEHPWL 458
 Db 243 DQPMFRRIILNCEYYFISPMWDEVSILNAKDLVKKLIVLDPKERLTTQALQHPWV 296

Query Match 13
 Best Local Similarity 39.8%; Score 534.5; DB 1; Length 474;
 Matches 117; Conservative 52; Mismatches 104; Indels 21; Gaps 3;

Qy 174 SDSLVDQDQTPYKDPDKK-----YIMSRPIGSAGEYKLAFOKSVCVKVAKIIS 224
 Db 43 SSVSSTSNEHPIVDPSKRDPLSDFPEVESELGRGATSYVRCKQKGTKQYALKVLY 102
 Qy 225 KRFKFKNTSNEHPIVSVDTEILKQKDPDKCIIENPDSDFYYVTEILMEGGELFDR 284
 Db 103 KTVDDKK-----IVRTETGIVLRLSHPNIIKLEIETPEISLVLVLTGGELFDR 153
 Qy 285 VNSTRTRREPPIAKLYFYQMLLAQYIHLGNGVTHRLDPKENVILSSTSSECCIIKTDGQS 344
 Db 154 IVEKGYYSSRDAADAVQKQLEAYLHENGIVRDLRPNLYATPAPDAPKIAIDGLS 213
 Qy 345 KILGETSLMRLTLCGTPYIAPAEVINTAGTCGSSAADCWLSGVILFVLCGYPFPSEQNS 404
 Db 214 KTEHQVNLMTKTVCTPGCPTLRGQ--AVGPEVDMWSVGLTGYIILCPFPYDVRG 270
 Qy 405 NIPLKQNLQAGKTYIAAWRNVSEQADLVRKNLVVDPEQRLTQKALEHPWL 458

Query Match 14
 Best Local Similarity 39.8%; Score 531; DB 1; Length 473;
 Matches 113; Conservative 48; Mismatches 96; Indels 12; Gaps 2;

Qy 190 DRYIMSPPIGSAGCDEVYKLAFOKSVCVKVAKIISRKFKONTSSNEHPIVDTEILK 249
 Db 44 DEFEVESELGRGATSYVRCKQKGTKQYALKVLTVDKK-----IVRTETGVLL 94

Query Match 15
 Best Local Similarity 42.0%; Pred. No. 2.3e-17;
 Matches 113; Conservative 48; Mismatches 96; Indels 12; Gaps 2;

Qy 250 KLDHPCLIKIENFFDSEDFYYVTEILMEGGELFDRVNNSTRREPPIAKLYFYQMLLAQY 309
 Db 95 RLSPHPNIKLEIETPEITSLVLEVLTGGELFDRVKEKGYSERADAVYKQILLEAVY 154

Query Match 16
 Best Local Similarity 42.0%; Pred. No. 2.3e-17;
 Matches 113; Conservative 48; Mismatches 96; Indels 12; Gaps 2;

Qy 310 LHENGVHRLDKPENVLLSSTSSECCIIKTDGQSILGETSLMRILCCTPTYLAPEVILN 369
 Db - - - - - 155 LHENGVHRLDKPENVLLSSTSSECCIIKTDGQSILGETSLMRILCCTPTYLAPEVILN 214

Query Match 17
 Best Local Similarity 42.0%; Pred. No. 2.3e-17;
 Matches 113; Conservative 48; Mismatches 96; Indels 12; Gaps 2;

Qy 370 TAGTGYSSAVDCWSGIVLPCLGCGYPPFSEQNSIPLKNOIAEGRKTYIAAWRNVSE 429
 Db 215 GC--AYGPEVDMWSVGLTGYIILCPFPYDVRGQFMFRRLNCEYYFISPMWDEVS 271

Query Match 18
 Best Local Similarity 42.0%; Pred. No. 2.3e-17;
 Matches 113; Conservative 48; Mismatches 96; Indels 12; Gaps 2;

Qy 430 QAFDLYKNLIVYDPEQRLTQKALEHPWL 458
 Db 272 NAKDLVRLIVLDPKERLTTQALQHPWV 300

RESULT 14

A;Cross-references: FlyBase:FBgn0011754
 A;Map position: 10
 C;Superfamily: protein kinase homology
 C;Keywords: phosphotransferase
 F;21-291/Domain: protein kinase homology <KIN>

Query Match 18.7%; Score 506; DB 2; Length 560;
 Best Local Similarity 35.0%; Pred. No. 3.7e-16;
 Matches 116; Conservative 57; Mismatches 134; Indels 24; Gaps 7;

Qy 186 KDFIDKYMIRPPIGGAGCDEVKLAQFQSKVCKAVKIKISKRKFKMNTSSNEHPTISVDT--
 Db 17 KGPYAKYKEPKELGRGIISSVRCIEKEKGKEFAAKIIDIGATESGEINPYHMLEATRQ 76

Qy 244 EIEETLKK-LDHPCTIKIENFFDSEDFYYIVLEMEGELFDRVNVNSTLREPIAKYLFYQ 302
 Db 77 EISIQRQVMGHPYIILQDVFESDAFVFLFELCPGELEDYLTSVTVLSEKKCPTIMRQ 136

Qy 303 MLLAVQYLHENGVIHRDLKPEBNVILSTSBECCCIKITDEGOSKILGETSLMRTLCGTPTY 362
 Db 137 IFEQEYEHIAKSTIVRDLKPEBNILL--DENHNVYKTDFAKAVARGREITNLCTPGY 193

Qy 363 LAPEVINT--AGTGYSSAVDCWSLGVILFVCLGCPPSEBQNSNIPKNOIAKSKYTY 419
 Db 194 LAPETIKCNCMFEGSGSQSEVDINAGVIMFTLJVGCPPWHRKQMVMLRN-IMGKYSF 252

Qy 420 IAAAWRNVSEQAFLIVKNLIVVDPFQLRITKQALIHPWLODDSMRKHTRVERLMYGDHTMP 479
 Db 253 TSPEWADISEDPKDILRKCLVLPDPSQRITYKEVLRHPFN-----QMVLMGDRRHPA 304

Query Match 18.7%; Score 507.5; DB 2; Length 735;
 Best Local Similarity 35.7%; Pred. No. 4.1e-16;
 Matches 128; Conservative 49; Mismatches 129; Indels 8; Gaps 12;

Qy 171 FVFSDLISVDD-----QTYPKD--FIDKYIMSRPIGGACDEVKLAQFQSKV 214
 Db 381 FVATGIMEDSKSPRATOAPLHSVQOHLHGKQNLVFSQYVKTGQVSYVCKRVHKAT 440

Qy 215 CKVKVAKVLI-SKRKFKRNTSSNEHPTISVDTDEIILKKL-DHPCIIKLENFPFSEDFYYIVL 273
 Db 441 NMEYAKVVDK-----SKRDP--SEEIEILLYRQGOHENITLKDYYDDSKHVVLYT 489

Qy 274 ELMEGGELFDRVNVNSTLREPIAKYLYQMLIAVQYLHENGVIHRDLKPEBNVLLSSTSE 332
 Db 490 ELMRGGELLDKILRQKPFSEBSFVLYTISKTVYLHSQVVRDLKPSNLVYDEGN 549

Qy 333 ECCCCIKITDEGOSKIL-GETS1MRTLQGTPYLAPEVLTNTAGTTGQSSAVDCWSLGVILFY 391
 Db 550 PEGLRICDFGFKQRLAENGQMLTPCYANFVAPETLK--RQGIDBEGCDWLSGVLYLT 606

Qy 392 CICGGYPFSEQNSNIP--LKRQIAEGKTYTAAAWRNVSQAFDLYKNULVDPFQLIT 449
 Db 607 MLAGYTFANGS5DTPBEILTRISSGKFTLSSGNNNTVSETAKDLYKSMHLHDPHORLTA 666

Qy 450 KOALEHFW-----LQDDSMKHTVERLIMYG-----VHDTMP---PPIKKNTRK 490
 Db 667 KQVLFQHFWITQDKDLPQLSQLSHQDLQLVKGMAATYSALESSSSKPTPQLKPIESSILAQR 725

Search completed: July 7, 2005, 13:03:00
 Job time : 43 secs

RESULT 15

S51600 phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Aug-2004
 C;Accession: S51600
 R;Bahr, S.M.; Chia, W.
 Mol. Gen. Genet. 245, 588-597, 1994
 A;Title: DPK-*gamma*, a putative *Drosophila* kinase with homology to vertebrate phosphorylants.
 A;Reference number: S51600; MUID:95107257; PMID:7808409
 A;Accession: S51600
 A;Molecule type: DNA
 A;Residues: 1-560 <BAH>
 A;Cross-references: UNIPROT:Q9YXV7; EMBL:U13014; NID:9311470; PMID:AAA64560.1; PID:5314
 A;Note: the authors translated the codon CAT for residue 528 as Ala and CAC for residue
 C;Generics:
 A;Gene: FlyBase:PhK-gamma

Scoring table:	BLOSUM62	Gapext	0.5	SUMMARIES		
Searched:	1612378 seqs, 512079187 residues					
Total number of hits satisfying chosen parameters:	1612378					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	UniProt_03:*					
	1: uniprot_sprot:*					
	2: uniprot_trembl:*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
RESULT 1	Q918V3	PRELIMINARY;	PRT;	517 AA.		
	ID: Q918V3;					
	AC: Q918V3;					
	DT: 01-OCT-2000 (TREMBLrel. 15, Created)					
	DT: 01-OCT-2000 (TREMBLrel. 15, Last sequence update)					
	DT: 01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
	DE: Protein kinase Cds1.					
	GN: Name=Cds1;					
	OS: Xenopus laevis (African clawed frog)					
	OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;					
	OC: Xenopodidae; Xenopus					
	OX: NCBI_TaxID:8355;					
	RN: [1]					
	RP: SEQUENCE FROM N.A.					
	RX: MEDLINE=20255236; PubMed=10793133;					
	RA: Guo Z., Dunphy W.G.;					
	RT: "Response of Xenopus Cds1 in cell-free extracts to DNA templates with double-stranded ends."					
	RT: RT					
	RL: Mol. Biol. Cell 11:1535-1546(2000)					
	CC: -- SIMILARITY: Belongs to the Ser/Thr protein kinase family.					
	DR: EMBL; AET174295; AAF58291; -.					
	DR: HSSP; 096017; IGC.					
	DR: GO; GO:0005524; F:ATP binding; IEA.					
	DR: GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.					
	DR: GO; GO:0016740; F:transferrase activity; IEA.					
	DR: GO; GO:0006468; F:protein amino acid phosphorylation; IEA.					
	DR: InterPro; IPR002553; PFA.					
	DR: InterPro; IPR010019; Kinase like.					
	DR: InterPro; IPR007119; Prot kinase.					
	DR: InterPro; IPR002290; Ser_Thr_Pkinase.					
	DR: SMART; SM00240; PFA; 1.					
	DR: InterPro; IPR002711; Ser_thr_Pkin_A.					
	DR: Pfam; PF00498; PFA; 1.					
	DR: Pfam; PF00659; Pkinase; 1.					
	DR: Prodrom; PD000001; Prot kinase.					
	DR: SMART; SM00240; PFA; 1.					
	DR: PROSITE; PS50006; PFA DOMAIN; 1.					
	DR: PROSITE; PS500011; PROTEIN KINASE DOMAIN; 1.					
	DR: PROSITE; PS50008; PROTEIN KINASE_SP; 1.					
	KW: ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.					
	SQ: SEQUENCE 517 AA; 58261 MW; 39DC06689090DB19 CRC64;					
Qy	1 MMSRDKTKESESQSOGTSSSSSSAPQSYSSQSSSSCTLSSLDTVPYQDLASIPEDPIDIED 60					
	Best Local Similarity 100.0%; Pred. No. 1.4e-164; Mismatches 517; Conservative 0; Indels 0; Gaps 0;					
Db	1 MMSRDKTKESESQSOGTSSSSSSAPQSYSSQSSSSCTLSSLDTVPYQDLASIPEDPIDIED 60					
Qy	61 IPQPMGRLWALKGFFLNHDCLHEEYVGRDKKKCDYTFDIPVLNQTTRYKTSKRHRIFQ 120					

Db	61	IQPGWGRWLWALGKGFLNHDCLHEEYVFGRKCDTFFDIPVLNQFDRYKTYSKRHFIFQ	120	Query Match Similarity 99.7%; Score 2704; DB 2; Length 517;
Qy	121	ELGHGHSRVAILEDLSGNGTFVNKEIGKRTPLTNNAAEALSLSPTNKVFVFSLSVDD	180	Best Local Similarity 99.8%; Pred. No. 4.5e-164; Mismatches 516; Conservative 0; Gaps 0;
Db	121	ELGHGHSRVAILEDLSGNGTFVNKEIGKRTPLTNNAAEALSLSPTNKVFVFSLSVDD	180	Matches 1 MMSRDTKTESQQOSGTTSSSSAPOSYSQSSSSGTLSSLDTPVQDLASIPEDPEIDED 60
Qy	181	QTIYPDFIDKYIMSPRIGSAGCEYKLAQKSVCCKVAKVLIISRKFKNTSSNEHPIS	240	Matches 1 MMSRDTKTESQQOSGTTSSSSAPOSYSQSSSSGTLSSLDTPVQDLASIPEDPEIDED 60
Db	181	QTIYPDFIDKYIMSPRIGSAGCEYKLAQKSVCCKVAKVLIISRKFKNTSSNEHPIS	240	Qy 61 1PQPGWRLWALGKGFLNHDCLHEEYVFGRKCDTFFDIPVLNQFDRYKTYSKRHFIFQ 120
Qy	241	VDTEIELLKUDHPCTIKENIFFDSEDFYXIVLMEGGELFDRVNSTRREPALKYF	300	Db 61 1PQPGWRLWALGKGFLNHDCLHEEYVFGRKCDTFFDIPVLNQFDRYKTYSKRHFIFQ 120
Db	241	VDTEIELLKUDHPCTIKENIFFDSEDFYXIVLMEGGELFDRVNSTRREPALKYF	300	Qy 121 ELGHGHSRVAILEDLSGNGTFVNKEIGKRTPLTNNAAEALSLSPTNKVFVFSLSVDD 180
Qy	301	YQMLAVQYLHENGVTHRDLPENVLSSTEBCC1KITFGQSKLGEISLMRTLCGTP	360	Db 121 ELGHGHSRVAILEDLSGNGTFVNKEIGKRTPLTNNAAEALSLSPTNKVFVFSLSVDD 180
Db	301	YQMLAVQYLHENGVTHRDLPENVLSSTEBCC1KITFGQSKLGEISLMRTLCGTP	360	Qy 181 QTIYPDFIDKYIMSPRIGSAGCEYKLAQKSVCCKVAKVLIISRKFKNTSSNEHPIS 240
Qy	361	TYLAPEVLNTAGTTGNSAVDWSLGVILFVCLGYGPPFSQNSNIPLQRQIAEGKTYI	420	Db 181 QTIYPDFIDKYIMSPRIGSAGCEYKLAQKSVCCKVAKVLIISRKFKNTSSNEHPIS 240
Db	361	TYLAPEVLNTAGTTGNSAVDWSLGVILFVCLGYGPPFSQNSNIPLQRQIAEGKTYI	420	Qy 241 VDTEIELLKUDHPCTIKENIFFDSEDFYXIVLMEGGELFDRVNSTRREPALKYF 300
Qy	421	AAAWRNVSEQAFLVNLVVDPEQLRTTQALEHPWLQDDSMRHTVERLVMYGVDTMPP	480	Db 241 VDTEIELLKUDHPCTIKENIFFDSEDFYXIVLMEGGELFDRVNSTRREPALKYF 300
Db	421	AAAWRNVSEQAFLVNLVVDPEQLRTTQALEHPWLQDDSMRHTVERLVMYGVDTMPP	480	Qy 301 YQMLAVQYLHENGVTHRDLPENVLSSTEBCC1KITFGQSKLGEISLMRTLCGTP 360
Qy	481	PIKKNITRKGEHWDDQASTSSCSEILPTSAEKARR 517		Db 301 YLAPPEVLNTAGTTGNSAVDWSLGVILFVCLGYGPPFSQNSNIPLQRQIAEGKTYI 420
Db	481	PIKKNITRKGEHWDDQASTSSCSEILPTSAEKARR 517		Qy 361 YLAPPEVLNTAGTTGNSAVDWSLGVILFVCLGYGPPFSQNSNIPLQRQIAEGKTYI 420
				Db 421 AAAWRNVSEQAFLVNLVVDPEQLRTTQALEHPWLQDDSMRHTVERLVMYGVDTMPP 480
				Db 421 AAAWRNVSEQAFLVNLVVDPEQLRTTQALEHPWLQDDSMRHTVERLVMYGVDTMPP 480
RESULT 2				
Q98TWO		PRELIMINARY;	PRT;	517 AA.
AC	Q98TWO;			
DT	01-JUN-2001	(T-EMBLref. 17, Created)		
DT	01-JUN-2001	(T-EMBLref. 17, Last sequence update)		
DT	01-OCT-2003	(TrEMBLref. 25, Last annotation update)		
DE	Protein kinase Cds1.			
GN	Name=Cds1;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
OC	Xenopoda; Xenopus.			
OX	NCBI_TaxID=8355;			
RN				
RP	SEQUENCE FROM N.A.			
DT	01-JUN-2001	(T-EMBLref. 17, Created)		
DT	01-OCT-2003	(TrEMBLref. 25, Last annotation update)		
RA	Matsui T., Nakanishi M., Takisawa H.; Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RA	-1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
RA	EMBL: AF32574; AAG5884.1; -.			
DR	GO; GO:000524; F:ATP binding; IFA.			
DR	GO; GO:001674; F:protein serine/threonine kinase activity; IFA.			
DR	GO; GO:0016740; F:protein amino acid phosphorylation; IFA.			
DR	GO; GO:000524; F:ATP binding; IFA.			
DR	InterPro; IPR00253; FHA.			
DR	InterPro; IPR01109; Kinase like.			
DR	InterPro; IPR00019; Prot_kinase.			
DR	InterPro; IPR00229; Ser_Thr_pk kinase.			
DR	InterPro; IPR008271; Ser_cbr_pk kinase.			
DR	InterPro; IPR008384; SMAD_FHA.			
DR	Pfam; PF00498; FHA; 1.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	ProDom; PD00001; Prot_kinase; 1.			
DR	SMART; SM00240; FHA; 1.			
DR	SMART; SM00220; S_TK; 1.			
DR	PROSITE; PSS0006; FHA_DOMAIN; 1.			
DR	PROSITE; PS0011; PROTEIN_KINASE; 1.			
DR	ATP-binding Kinase; Serine/threonine-protein kinase; Transferase.			
KW	SEQUENCE 517 AA; 58310 MW; 401A323AA0BDCSB CRC64;			
RN				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9905399; PubMed=9836640; DOI=10.1126/science.282.3395.1893;			
RA	Matsuoka S., Huang M., Elledge S.J.;			
RA	McGowan C.H.; "A human homologue of the checkpoint kinase Cdk2 protein kinase Cdk2." Science 282:1893-1897(1998).			
RA	Linkage of ATM to cell cycle regulation by the Cdk2 protein kinase Cdk2." Curr. Biol. 9:1-10(1999).			
RN				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9908110; PubMed=9889122; DOI=10.1016/s0960-9882(99)80041-4;			
RA	Blasina A., van de Weyer I., Laus M.C., Luyten W.H.M.L., Parker A.E.,			
RA	McGowan C.H.; "A human homologue of the checkpoint kinase Cdk2 protein kinase Cdk2." Curr. Biol. 9:1-10(1999).			
RN				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9905399; PubMed=9836640; DOI=10.1126/science.282.3395.1893;			
RA	Matsuoka S., Huang M., Elledge S.J.;			
RA	McGowan C.H.; "A human homologue of the checkpoint kinase Cdk2 protein kinase Cdk2." Science 282:1893-1897(1998).			
RN				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99199255; PubMed=10097108; DOI=10.1073/pnas.96.7.3745;			
RA	Brown A.L., Lee C.-H., Schwarz J.K., Mitiuk N., Pwniccia-Worms H.,			

Db	387	LCGPPTYLAPEVLSINGTAGYSRAVDCKMSLGVTLFICLSTGYPPFSEHKTQVSILKDQITSG	446	CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	416	KTYTAAWRNVSQAFDVKLNUVDPBQLRQLTKOALBHPWQDDSMKHTVERLGYVD	475	CC
Db	447	KYNLIPETWVTDVSBKALDVKLNUVDPBQLRQLTEALSHPWLQDEMKKKFQDLVQEK	506	CC
Qy	476	HTMPPI-KKNLTKRKGHEWD-QDASPTP-----CSETL	507	CC
Db	507	NLVBLPLPAAQTSGQRPIDELEADAESSKRLAVCKAVL	545	CC
RESULT 5				
CHK2_MOUSE	CHK2_MOUSE	STANDARD;	PRT;	546 AA.
AC	Q92265;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Serine/threonine-protein kinase Chk2 (EC 2.7.1.3.7).			
GN	Name=Chk2; Synonyms=CHK2, Rad53;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX				
RN	[1]			
SEQUENCE FROM N.A.				
RX	Matsuoka S., Huang M., Ellledge S.J.;			
RT	"Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";			
RN	Science 282:1893-1897 (1998).			
RN	[2]			
SEQUENCE FROM N.A.				
RC	STRAIN=MR1; TISSUE=Mouse mammary gland;			
RC	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Colkins F.D., Buetow K.H., Scheuler G.D.,			
RA	Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Shapleyton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rosa S.A., McQuillan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	McEwan P.J., McKernan K.J., Malek J.A., Gundarathne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Murzina K., Farmer A.A., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahay J., Helton E., Kettman M., Madan A., Casavant T.L., Scheetz T.E.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,			
RA	Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
CC	-I- FUNCTION: Controls cell cycle checkpoint. May participate in transduction of the DNA damage and replicational stress signals.			
CC	CC Inhibits CDC25 phosphatase by phosphorylating it, preventing the entry into mitosis. May have a role in meiosis as well.			
CC	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	-I- ENZYME REGULATION: Kinase activity is up-regulated by autophosphorylation. Rapidly phosphorylated in response to DNA damage and to replication.			
CC	-I- SUBCELLULAR LOCATION: Nuclear.			
CC	-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1 subfamily.			
CC	-I- SIMILARITY: Contains 1 FHA domain.			
This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial			
Qy	485	NIRKRGHEWDQDASTSS-----CSEI	507	RESULT 6
Db	606A11			
Qy	519	TSSQRPLLEVEGMPSIKRLSVCAGV	546	

DT	05-JUL-2004 (TREMBLrel. 27, Created)	Qy	230 MNTSSNEHP-LSVDPTEIEILKKLDHPCIIKIKENPFDSEDFFYIVLELMEGGELFDDEVNNS 288
DT	05-OCT-2004 (TREMBLrel. 28, Last annotation update)	Db	301 IGSAREADPAINVETIEILKKLNFICIKIKNPFDAE-YYTIVELMEGGELFDKVGNS 359
DE	Protein kinase Chk2 transcript variant insX (CHEK2 protein).	Qy	289 TRLEPDIAKLKYFYQMLLAVOYLHENGVIHDLKPENVLSSTEBCIKITDFQSKILG 348
GN	Name=CHK2; Synonyms=CHEK2;	Db	360 KRLKEATCKLYPYQMLLAVOYLHENGVIHDLKPENVLSSQEDOLIKITDFQSKILG 419
OS	Homo sapiens (Human)	Qy	349 ETSIMLTCGTPYTLAPEVINTAGTGYSSAVDCMSLGTVLFCGYPPFSEONSNIPL 408
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;	Db	420 ETSIMLTCGTPYTLAPEVINTAGTGYSSAVDCMSLGTVLFCGYPPFSEHRTQVSL 479
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy	409 KNOIAEGKTYIAAWRNTVSEAFDLYKLNLYVDPBQLRTTKQALEHPMLQDDSMKHTVE 468
OX	NCBI_TaxID=9606;	Db	480 KDQITSGKCNFIPWAEVSEKALDVKLUVVDRKARFTEBALHPWLODEDKRKFO 539
RN	SEQUENCE FROM N.A.	Qy	469 RLMYGDHTMPP--IKNNTIRKGHEWQDASTSS---CSETL 507
RC	TISSUE=Breast carcinoma;	Db	540 DLLSEENESTALPOVLAQPSLTSRKFRREGAEATTKRPAVCAAWL 586
RA	Staaliesen V.; Palk J.; Geisler S.; Bartkova J.; Borresen-Dale A.-L.,	Qy	
RA	Lillehaug J.R.; Lønning P.E.;	Db	
RA	Collins J.B.; Wright C.L.; Edwards C.A.; Davis M.P.; Grinham J.A.,	Qy	
RA	Cole C.G.; Goward M.E.; Aguado B.; Malliva M.; Mokrab Y.; Huckle B.J.,	Db	
RA	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.	Qy	
RA	Beare D.M.; Dunham I.; Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	Db	
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	RESULT 7	
DR	EMBL; AY551197; AAS5458.1; -.	Q9HC08	PRELIMINARY;
DR	EMBL; CR456118; CAG30304.1; -.	ID	PRT; 514 AA.
DR	HSSP; Q63450; 1A06.	AC	Q9HC08;
DR	GO; GO:000524; F:ATP binding; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DR	GO; GO:0016740; F:transferase activity; IEA.	DR	DB (Protein kinase Chk2 transcript variant del19) (Fragment).
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.	GN	Name=Chk2; Synonyms=CHK2;
DR	InterPro; IPR000253; PHA.	OS	Homo sapiens (Human).
DR	InterPro; IPR011009; Kinase like.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	InterPro; IPR000719; Ser_Thr kinase.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR	InterPro; IPR002290; Ser_Thr kinase.	OX	
DR	InterPro; IPR005271; Ser_Thr_protein_AS.	RN	
DR	InterPro; IPR008984; SMAD PHA.	RA	Ogawa A.; Okabe-Nakamura A.;
DR	InterPro; IPR001245; Tyr_D kinase.	RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR	Pfam; PF000498; PHA; 1.	RL	[2]
DR	Pfam; PF00069; Pkinase; 1.	RN	SEQUENCE FROM N.A.
DR	ProDom; PD000001; Prot_kinase; 1.	RP	
DR	SMART; SM00240; FHA; 1.	RC	SEQUENCE FROM N.A.
DR	SMART; SM00220; S_TKc; 1.	RA	TISSUE=Breast carcinoma; Bartkova J.; Bartkova J.; Borresen-Dale A.-L.,
DR	SMART; SM00219; TYRKc; 1.	RA	Staalesen V.; Falck J.; Geisler S.; Bartkova J.; Borresen-Dale A.-L.,
DR	PROSITE; PS00006; FHA DOMAIN; 1.	RA	Lukas J.; Lillehaug J.R.; Lønning P.E.;
DR	PROSITE; PS00011; PROTEIN KINASE DOMAIN; 1.	RA	Submitted (FEB-2004) (TREMBLrel. 27, Last annotation update)
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	DR	DB (Protein kinase Chk2 transcript variant del19) (Fragment).
DR	ATP-binding; Kinase; Serine/threonine_protein kinase; Transferase.	DR	EMBL; AB0-105; BAB17231.1; -.
KW	SEQUENCE 586 AA; 6518 MW; 55BDE42C9A0F98A7 CRC64;	DR	EMBL; AY551299; AAS58460.1; -.
SQ	59.9%; Score 1624; DB 2; Length 586;	DR	DR; GO:0005524; F:ATP binding; IEA.
Matches 326; Conservative 74; Mismatches 105; Indels 8;	DR	DR; GO:0004672; F:protein kinase activity; IEA.	
DR	SMART; SM00240; FHA; 1.	DR	DR; GO:0004648; F:protein amino acid phosphorylation; IEA.
DR	SMART; SM00220; S_TKc; 1.	DR	DR; GO:0006468; F:protein kinase like.
DR	SMART; SM00219; TYRKc; 1.	DR	DR; GO:0001009; Kinase like.
DR	PROSITE; PS00006; FHA DOMAIN; 1.	DR	DR; PROSITE; IPR001009; Kinase like.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	DR	DR; PROSITE; IPR001019; Prot_kinase.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	DR	DR; PROSITE; IPR008984; SMAD_FHA.
DR	ATP-binding; Kinase; Serine/threonine_protein kinase; Transferase.	DR	Pfam; PF00498; FHA; 1.
DR	SEQUENCE 586 AA; 6518 MW; 55BDE42C9A0F98A7 CRC64;	DR	DR; PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	586 AA; 6518 MW; 55BDE42C9A0F98A7 CRC64;	KW	Kinase.
DR	586 AA; 6518 MW; 55BDE42C9A0F98A7 CRC64;	FT	NON_TER 514
DR	586 AA; 6518 MW; 55BDE42C9A0F98A7 CRC64;	SQ	SEQUENCE 514 AA; 57525 MW; 8B9B81830B8032F CRC64;
DR	121 LSSDPPASASQAGITGRVRRHPRPVCSLKCVCNDYWFGRKSCYCFCDEPILKRTDKYR 180	Query Match	55.3%; Score 1499; DB 2; Length 514;
DR	110 TYSKHFRIQFQEGHGHRSR VANTELDGGNTGTFVNLKELIGKRTPLTNNAETALSLPTNK 169	Best Local Similarity	55.5%; Pred. No. 2.6e-87;
DR	61 SSLETVSTQELYSIPEQDQEPEPPTPAPWARIQDGFANLTTESGHVTQSDLEI 120	Matches 302; Conservative 72; Mismatches 102;	Matches 302; Mismatches 102; Mismatches 102; Mismatches 102;
DR	80 -----CLHEEYFGDKKCDYTFDIPVLNQSTDYK 109	2 M8RDTKIESQ-----	-QSGTSSSSSSSSAP-QSYVSQSSSSGTL 37
DR	170 VPFVFSDLSSVDDOTIYKDFIDKYMSPBPGSACGEYKLAFKSVCXKVAIKIISRKFK 229	Db	1 M8RDTKIESQ-----
DR	241 VVFEDLTVDDQSVPKALRDEXTMSKTLGKGRPLANNSETALSLSRNK 300	Qy	1 NSRSEDEAQOSHGSACQPHGSVTQSGSSSSQSGGSSSSSTSPNSSQSSHSSSGTL 60

RA	Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.;	475	NPMPREFAETRK	486
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=AB; TISSUE=Whole body;			
RC	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
RA	1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
RA	EMBL: BC044519; AAH44519.1; - .			
RA	HSSP: P49137; 1NXX.			
RL	ZFIN: ZDB-GENE-010131-8942; ZGC:55865.			
CC	GO: GO:000554; P:ATP binding; IEA.			
CC	GO: GO:004674; P:protein serine/threonine kinase activity; IEA.			
CC	GO: GO:001640; P:transferase activity; IEA.			
CC	GO: GO:006468; P:protein amino acid phosphorylation; IEA.			
CC	InterPro: IPR00253; PHA.			
DR	InterPro: IPR01100; Kinase_like.			
DR	InterPro: IPR000719; Prot_kinase.			
DR	InterPro: IPR002290; Ser_Fhr_pk kinase.			
DR	InterPro: IPR00271; SerThr_pkin_AS.			
DR	InterPro: IPR008384; SMAD_FHA.			
PFam	PF00498; PHA; 1.			
PFam	PF00659; Pkinase; 1.			
PFam	PF00240; EHA; 1.			
DR	SMART; SMART_000220; S_TKc; 1.			
DR	PROSITE; PS50006; FHA DOMAIN; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS50108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding Kinase; Serine/threonine-Protein kinase; Transferase.			
SQ	SEQUENCE 503 AA; 56657 MW; 351A24EA5BBAF8D5 CRC64;			
Qy	3 SRDTKTESQ-QSGCTSSSSSSAPOSQYQ-SSSSGRLSSLDTPVQDIAISPDEIDE 59	120	QELQGHGHSRVAINTERDLSGNGTFTYKEIGKRTPLTNNAEIALSLPTNKVFVFSLSDV 179	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	8 SGEQSQTSQTOSQPSQSSAAPTSSQGSSSSGTLSVDTVQELQSIPDEEE-E 65	126	RD----ENLVYLEDLSGNGTWDKELGNGKOSLGLGNSVIALAQHQVMFIDKAD 180	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	60 DIPQPGWQIWLQKGFNLAHDCLHEBYVFRGKCDYTFDPIVANQTDRYKTYSKRHFRT 119	180	DQTTPKDFDKYIMSRPFGGAGCEVKLAQFSVKCKEVAKVLLKSKRKF-KXNTSSNNEHP 238	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Db	66 VQQVWGRTPILKQGFSVNCTENOYFCRDRKCDYSESNNILKKSPPVNTYSKRHFRT 125	181	DOANPLPEFSKTYIARKIGTG/CGEVKLVAEKEFKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Qy	120 QELQGHGHSRVAINTERDLSGNGTFTYKEIGKRTPLTNNAEIALSLPTNKVFVFSLSDV 179	182	ISVDTIEILKDHPC1IKENNFEDSEPFYVLEMEGLPFDVNRNSTREPIAKL 298	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	126 RD----ENLVYLEDLSGNGTWDKELGNGKOSLGLGNSVIALAQHQVMFIDKAD 180	183	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	180 DQTTPKDFDKYIMSRPFGGAGCEVKLAQFSVKCKEVAKVLLKSKRKF-KXNTSSNNEHP 238	184	ISVDTIEILKDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	184 DQTTPKDFDKYIMSRPFGGAGCEVKLAQFSVKCKEVAKVLLKSKRKF-KXNTSSNNEHP 238	185	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	185 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	186	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	186 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	187	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	187 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	188	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	188 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	189	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	189 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	190	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	190 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	191	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	191 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	192	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	192 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	193	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	193 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	194	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	194 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	195	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	195 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	196	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	196 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	197	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	197 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	198	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	198 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	199	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	199 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	200	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	200 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	201	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	201 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	202	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	202 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	203	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	203 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	204	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	204 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	205	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	205 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	206	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	206 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	207	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;
Db	207 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	208	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Query Match 48.4%; Score 1311.5; DB 2; Length 503;
Qy	208 YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	209	YIAERIEILKKIDHPC1IKEYTKEVKKVLTINCHDFFSIGPATR--- 237	Best Local Similarity 53.2%; Pred. No. 2.2e-75; Mismatches 264; Conservative 84; Gaps 7;

Qy	332	EECCIKITDQGSKILGETSLMRTLCLGTPPTYLAPAEVINTAGTGYSSAVDCMSLGVILFV	391	Qy	433	DIVKNNLIVDPEQRLTKQALEHPWILQDDSMKHTVRLMYGVDHTMPP---IKKNIRK 489
Db	269	EDCLIKITDQGHSKILGETSLMRTLCLGTPPTYLAPAEVINTAGTGYSSAVDCMSLGVILFV	328	Db	240	DIVKNNLIVDPEQRLTKQALEHPWILQDDSMKHTVRLMYGVDHTMPP---IKKNIRK 299
Qy	392	CLCGYPPEQNSNIPKLKNQIAECKYTYAAWNRVNEQAFDLVKNLIVDPEQRLTTKQ	451	Qy	490	RGEHWDODASTS---CSETL 507
Db	329	CLSGYPPEFHRQVSLKDQITSGKYNFPEWAEVSKALDLVKKLIVDPEKFTTE	388	Db	300	RPREGEAEGAEETTKRPAVCAVL 322
Qy	452	ALRHPWLOPDSMFTVRLMYGVDHTMPP---IKKNIRKRGHEWDODASTS---C	503	RESULT 12		
Db	389	ALRHPWLOPDSMFTVRLMYGVDHTMPP---IKKNIRKRGHEWDODASTS---C	448	Q6QA08		
Qy	504	SEIL 507		Q6QA08	PRELIMINARY;	PRT;
Db	449	AAVL 452		Q6QA08	PRELIMINARY;	PRT;
Q9HBS5		Q9HBS5; PRELIMINARY;	322 AA.	Q6QA08	PRELIMINARY;	PRT;
AC		Q9HBS5;		Q6QA08	PRELIMINARY;	PRT;
DT	01-MAR-2001	(TREMBLrel. 16, Created)		Q6QA08	PRELIMINARY;	PRT;
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		Q6QA08	PRELIMINARY;	PRT;
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		Q6QA08	PRELIMINARY;	PRT;
DE		Hypothetical protein.		Q6QA08	PRELIMINARY;	PRT;
OS		Homo sapiens (Human).		Q6QA08	PRELIMINARY;	PRT;
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Q6QA08	PRELIMINARY;	PRT;
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Q6QA08	PRELIMINARY;	PRT;
OX		Q9HBS5 (TaxID:9606);		Q6QA08	PRELIMINARY;	PRT;
RN		[1] SEQUENCE FROM N.A.		Q6QA08	PRELIMINARY;	PRT;
RP		SEQUENCE FROM N.A.		Q6QA08	PRELIMINARY;	PRT;
RA		RA J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,		Q6QA08	PRELIMINARY;	PRT;
RA		Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,		Q6QA08	PRELIMINARY;	PRT;
RA		Yu J., Han L.H.,		Q6QA08	PRELIMINARY;	PRT;
RA		Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		Q6QA08	PRELIMINARY;	PRT;
CC		-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		Q6QA08	PRELIMINARY;	PRT;
DR		EMBL; AF217975; AA617290; AA617218.1; -.		Q6QA08	PRELIMINARY;	PRT;
DR		HSSP; P49137; INXK.		Q6QA08	PRELIMINARY;	PRT;
DR		GO; GO-0005524; F:ATP binding; IEA.		Q6QA08	PRELIMINARY;	PRT;
DR		GO; GO-004674; F:protein serine/threonine kinase activity; IEA.		Q6QA08	PRELIMINARY;	PRT;
DR		GO; GO-0016740; F:transfere activity; IEA.		Q6QA08	PRELIMINARY;	PRT;
DR		GO; GO-0006468; F:protein amino acid phosphorylation; IEA.		Q6QA08	PRELIMINARY;	PRT;
DR		InterPro; IPR00719; Prot kinase.		Q6QA08	PRELIMINARY;	PRT;
DR		InterPro; IPR000719; Prot kinase.		Q6QA08	PRELIMINARY;	PRT;
DR		InterPro; IPR002290; Ser_Thr_pk kinase.		Q6QA08	PRELIMINARY;	PRT;
DR		InterPro; IPR008271; Ser_Thr_pk kinase.		Q6QA08	PRELIMINARY;	PRT;
DR		ProDom; PD000001; Prot kinase; 1.		Q6QA08	PRELIMINARY;	PRT;
DR		SMART; SM00220; S_TK_C.		Q6QA08	PRELIMINARY;	PRT;
DR		PROSITE; PS000101; PROTEIN_KINASE_DOM; 1.		Q6QA08	PRELIMINARY;	PRT;
DR		PROSITE; PS000108; PROTEIN_KINASE_ST; 1.		Q6QA08	PRELIMINARY;	PRT;
DR		ATP-binding; Hypothetical_protein; Kinase;		Q6QA08	PRELIMINARY;	PRT;
KW		SERINE/threonine/protein kinase; Transferase.		Q6QA08	PRELIMINARY;	PRT;
SEQUENCE		322 AA; 36157 MW; D31257F4B9652438 CRC64;		Q6QA08	PRELIMINARY;	PRT;
Query Match		39.3%; Score 1066; DB 2; Length 322;		Q6QA08	PRELIMINARY;	PRT;
Best Local Similarity		63.8%; Pred. No. 5, 4e-60;		Q6QA08	PRELIMINARY;	PRT;
Matches 206; Conservative		44; Mismatches 63; Indels 10; Gaps 4;		Q6QA08	PRELIMINARY;	PRT;
SQ		HPC1IKIENFDSEDEFYVILMEGGELFDVYVNSTRLEPIYKLYFYQMLLAQVYLLHE 312		Q6QA08	PRELIMINARY;	PRT;
Qy	194	MSRPIGSACGGEYKLAFKRVSCKVAKIISKRKFKMNTSSNEHP-TISVDTBEIILKKLD 252		Q6QA08	PRELIMINARY;	PRT;
Db	1	MSKTLGSGACGBYKLAFKTCKVAKIISKRKFAISGARAEADPAVNEYTIEIIRKLN 60		Q6QA08	PRELIMINARY;	PRT;
Qy	253	HPC1IKIENFDSEDEFYVILMEGGELFDVYVNSTRLEPIYKLYFYQMLLAQVYLLHE 312		Q6QA08	PRELIMINARY;	PRT;
Db	61	HPC1IKIENFDSEDEFYVILMEGGELFDVYVNSTRLEPIYKLYFYQMLLAQVYLLHE 312		Q6QA08	PRELIMINARY;	PRT;
Qy	313	NGYTHRDIKPENVLSSTSCECCIKITDGFQSKILGETSLMRTLCLGTPPTYLAPEVINTAG 372		Q6QA08	PRELIMINARY;	PRT;
Db	120	NGIITHRDIKPENVLSSTSCECCIKITDGFQSKILGETSLMRTLCLGTPPTYLAPEVINTAG 379		Q6QA08	PRELIMINARY;	PRT;
Qy	373	TGYSAAVDCWSLGVILFVCLCGYPPEFSQNSNIPLKQKQIAECKYTYAAWRVNSEQAF 432		Q6QA08	PRELIMINARY;	PRT;
Db	180	TAGYNRAVDWSLGVILFICLGSYPPSEHRQVSLKDQITSGKYNFPEWAEVSEKAL 239		Q6QA08	PRELIMINARY;	PRT;
Qy		271 SVLBMGGELFDRVNNSTRLEPIAKLYFYQMLLAQVYLLHE 308		Q6QA08	PRELIMINARY;	PRT;
Qy		272 VLBMEGGELFDRVNNSTRLEPIAKLYFYQMLLAQVYLLHE 308		Q6QA08	PRELIMINARY;	PRT;
Qy		273 KTCKVAKIISKRKFAISGARAEADPAVNEYTIEIIRKLNHPC1IKNKFDAE-D-YYI 299		Q6QA08	PRELIMINARY;	PRT;

DR	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PFam; PF00098; FHA; 1.	
PFam; PF00089; Pkinase; 1.	
DR	SMART; SMART_00001; Prot_kinase; 1.
DR	SMART; SMART_00220; S_TKc; 1.
DR	SMART; SMART_00006; FHA; 1.
DR	PROSITE; PS00006; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
DR	PROSITE; PS00011; PROTEIN KINASE_ST; 1.
DR	PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR	Alternative splicing; ATP-binding; Nuclear protein; Serine/threonine-protein kinase; Transferase.
FT DOMAIN	69 129 Protein kinase.
FT DOMAIN	174 441 Protein kinase.
FT NP BIND	180 188 ATP (By similarity).
FT BINDING	203 203 ATP (By similarity).
FT ACT SITE	303 303 Proton acceptor (By similarity).
FT VARSPlicing	46 62 Missing (in isoform Short).
FT SEQUENCE	476 AA; 54261 MW; 58D583E015C4E626 CRC64;
Query Match	30.5%; Score 828; DB 1; Length 476;
Best Local Similarity	36.8%; Pred. No. 1.3e-4;
Matches 190; Conservative	90; Mismatches 162; Indels 74; Gaps 13;
Qy	2 MSRDTKTESQOSQGTSSSSAPOSYSQSSSGTSSLDTVPQDOLASIPEDPEIDED 61
Db	1 MARDT---QGTGT-----QSQSNNTQVQESPMKIV----- 31
Qy	62 POPWGRLLWALGKGP-----LNHDCLHEEYVGRDKKCDYTF---DI 99
Db	32 ---WGRLY---GRNKKIKSLGTSSKRYIYTHSSFSVDLNDEFTAGRGEANDLTLNDL 86
Qy	100 P---VLNQDTRYKTYSKHFRFQELGHHSRANTEDLSIGNTFVKEIIGKRTPLTN 157
Db	87 PEKILTR----ISKTHP---IKRANCELTNPVYIQDLRSRGTFTVNNKEIGTGNRBRILN 139
Qy	158 NAEIALSLPTNKVWVFSPLSVDDQDTIYPKDFDKYIMSRPIGSGACEVKLAFVK 217
Db	140 DIVISLSPHTYKAFVFDLSPNSIGDPEEINKRTYVNRKLGSGAYGLVRLVYDTRTCQ 199
Qy	218 VAVKIIISKRKFKF-MNTSSN-EHPISVDTIEIILKLDHPCLIKIENFFDSEDFYVYLE 275
Db	200 FAMKIVKKNMLSGARPNTFSPPDRVNEAKIMNLSPHCVYRMHDIVDSDVMTYLEF 259
Qy	276 MEGGELDPLVNRVSTRREPALKYFYONLILAYQLHENGWTHRDLPENVLSSSTBEC 335
Db	260 MRGGDLNRIISNKLLEDISKYFQMCHAVKYLHDGITHRDLKDPNVILTEIDETL 319
Qy	336 IKITDFFGOSKKGLETSLMRITLGCTPTYLPEVLYNTAGTGYSSAVDCWSAGVLFVCLCG 395
Db	320 LKVSDFGISKFKVQDSWMTLCTPLVAPPEVLTGREATTKVQD1WLSLAVLFTLGS 379
Qy	396 YPPFSEQNNSNIPNIKQIAEGKTYIAAWRNVSEAOFLVNLVLYDPEQBLTQALEH 455
Db	380 TLPLPSDEYGT-PAAQQLKKGRFAYGHPSWKSYSQSKRQLLIVPERRSIDVYQ 438
Qy	456 PWLQDDSSKRTVERLM-----YGVDTITMPPTPKR 485
Db	439 SWLRDAPMLQKAKRMLKDGMETEEENPLEPPTKRS 474
RESULT 14	
Q6QAA0	PRELIMINARY: PRT; 289 AA.
AC	Q6QAA0_0
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB	Protein kinase Chk2 transcript variant del17.
GN	Name=CHK2
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Metazoan; Chordate; Vertebrate; Euteleostomi; Craniota; Vertebrata; Eukaryota.
OX	NCBI_TaxID=5141;
RN	SEQUENCE FROM N.A.
RC	STRAIN=OR4A;
RA	Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA	Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA	Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA	Qui D., Ianakiev P., Pedersen E., Nelson M., Burnside M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeliter A., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA	Kamal M., Kamysyseleis M., Mauceli E., Bielke C., Rudd S., Prishman D.,	Db	532 IDSMLVVDPPEKRFITIDCLSHPWTQKTPGVNDSTNGLVNGIA-GLDVT-----RRGVLR 585
RA	Cogoni C., Macino G., Rasmussen R.L., Metzenberg D., Perkins D.D., Kroen S.,	Qy	489 KR 490
RA	Catchside D., Li W., Pratt R.J., Osmanni S.A.,	Db	586 ER 587
RA	Desouza C.C., Glies L., Orbach M.J., Berglund J., Voeleker R.,		
RA	Yarden O., Flammann M., Seiler S., Dunlap J., Radford A., Aramayo R.,		
RA	Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,		
RA	Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,		
RA	"The Genome Sequence of the Filamentous Fungus <i>Neurospora crassa</i> ."		
RT	RL Nature 0:0(2003)		
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		
CC	-1- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AABX01000031; EAA35234; 1; -		
DR	HSSP; P49137; INXK;		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0041674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR000253; FHA.		
DR	InterPro; IPR000253; FHA.		
DR	InterPro; IPR01109; Kinase like.		
DR	InterPro; IPR008271; Ser_Thr_protein_AS.		
DR	InterPro; IPR008984; SMAD_FHA.		
DR	Pfam; PF00498; FHA; 1.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	PROSITE; PS50006; FHA DOMAIN; 1.		
DR	PROSITE; PS00107; PROTEIN KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN KINASE_DON; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Hypothetical protein; Kinase;		
KW	Serine/threonine-protein kinase; Transferase.		
SQ	SEQUENCE 712 AA; 79186 MW; A5EA253542B339B CRC64;		
Query	26.8% Score 727.5; DB 2; Length 712;		
Best Local Similarity	32.8%; Pred. No. 5.4e-18;		
Matches	178; Conservative 95; Mismatches 168; Indels 101; Gaps 18;		
Qy	15 GTSSSSSSSAPQSYSSQSSSSGTLSSSDTPVYQVDLASTP-----DEBIDEDIPQ-FWGRU 68		
Db	81 GRPSQSQSPRENHQSQASQNLNTD----QAFSQQLPDLQKALSDDEVDEVKEGWGYL 137		
Qy	69 WALG-----KGLINHDOLHEE----- 84		
Db	138 FLDPRYGGRCVYVRLRAAACPLPDTYSQAVGSKRKGQKALIKEHDLTKVKGLPSG 197		
Qy	85 -YVFGDRDKCDYTFDIPVNLNQTDKYTSKRFRIQELIGHHSRYANIBDLSGNNTFVN 143		
Db	198 GYLIGHRHPEDCQIEDPIV-----SNRHCIIFFTE-NKGNDTIAVLEDLSSNGTFVN 247		
Qy	144 KELIGKERTPLPTNNAAATASLPTPNKVFPSLSDVDTQTYPKD-----FLDKYIMSRP1 198		
Db	248 EALVGRNRRRELQELDEAV-LGTR-FIYR-----TPKSRHTSAPFQQYTMQLQL 296		
Qy	199 GSGACGEVYKLAQFQSVCKKAVKIIISKRKFQNTTSNEPHISVDTIEELKKLDHPCLIK 258		
Db	297 GKGHFAEVYLCYEVKSTGTYQAYTKVFSKTPVGEERSIDE----GLQQEATAVLNGVSHPNVLC 353		
Qy	259 IENFFDSSDFYTYVLEMEGGEDFDRVNNSTLREPLAKLYFYQMLIAVQYLNHENGVIR 318		
Db	354 LKDTNEPNAVHLVLELAPGGELFNYLVKTKLISENECRLKFTQFOGVYLNHDNIVHR 413		
Qy	319 DIKPENVLLSSSEECCKIKTGFQSKLGETSLMRTLCGPTTYLAPEVNTAGTGYSS 378		
Db	414 DIKPENIL--VDDDLIVRVLADGLAKIGEESFTTLGTPSYVAEILTDTRHRYKTY 471		
Qy	379 AVDCWSLIGVLFVCLGCGYPPESEQ--NSNIP--LKNQIAEGKYTYIAAMRNNSQAFD 434		
Db	472 AVDWSLIGVVLICLCCGPFPFSDELTSPDFPSLSQDQIRGKFDYPSWVDFVDDIALDL 531		
Qy	435 VKNLLVNDPEQRLLTQKALEHPMLQ-----DDSMKTHTVERLMLYGDHTMPPPIKNNIR 488		

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 7, 2005, 12:33:18 ; Search time 162 Seconds

(without alignments)

1234.291 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQQSQGTTSSSS.....ASTSSCSEILPTSAEKRKRAKR 517

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : A_GenSeq_16Dec04;*

1: GenSeqDP1980s;*

2: GenSeqDP1990s;*

3: GenSeqDP2000s;*

4: GenSeqDP2001s;*

5: GenSeqDP2002s;*

6: GenSeqDP2003s;*

7: GenSeqDP2003bs;*

8: GenSeqDP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2712	100.0	517 5 AAB47789	Aab47789 Protein k
2	1656	61.1	542 4 AAG68375	Aag68375 Human Chk
3	1655.5	61.0	543 2 AAY06204	Aay06204 Human che
4	1655.5	61.0	543 2 AAT05765	Aat05765 Novel hum
5	1655.5	61.0	543 5 AAM48995	Aam48995 Human Chk
6	1655.5	61.0	543 5 ABG330701	Abg330701 Human che
7	1655.5	61.0	543 8 ADL12561	Adl12561 Human Chk
8	1655.5	61.0	543 8 ADM72213	Adm72213 Human TAS
9	1655.5	61.0	543 8 Ado44010	Ado44010 Amino aci
10	1651.5	61.0	543 8 ADQ09232	Adq09232 Human Chk
11	1643.5	60.9	543 5 AAM48996	Aam48996 Human cel
12	1643.5	60.6	543 3 AAY67968	Aay67968 Human cel
13	1624	59.9	586 8 ADN61455	Adn61455 Human KPP
14	1499	55.3	514 5 AAM48994	Aam48994 Human Chk
15	1499	55.3	514 8 ADL32563	Adl32563 Human Chk
16	838.5	30.9	459 4 ABG65298	Abg65298 Drosophila
17	621	22.9	513 8 ADN18925	Adn18925 Bacterial
18	603	22.2	356 4 AAB84360	Aab84360 Amino aci
19	600.5	22.1	355 4 AAB50055	Aab50055 Murine De
20	600.5	22.1	355 4 AAE11777	Aae11777 Human kin
21	600.5	22.1	355 4 AAM41268	Aam41268 Human pol
22	600.5	22.1	355 5 ABP0178	Abp0178 Human Cam
23	600.5	22.1	357 4 AAE11768	Aae11768 Human kin
24	600.5	22.1	357 8 ADJ75440	Adj75440 Marker ge
25	600.5	22.1	357 8 ADQ15044	Adq15044 Human can

ALIGNMENTS

RESULT 1
ID AAB47789 standard; protein; 517 AA.

XX AC AAB47789;
XX DT 04-MAR-2002 (first entry)
XX DB Protein kinase Cds1.
XX KW Protein kinase; Xenopus; Cds1; DNA damage checkpoint; cell cycle; Cdc25; forkhead-associated domain; FHA domain; ATM; ATR; DNA-PK; Chk2; human; mitotic; delay.
XX OS Xenopus laevis.
XX PN WO200183703-A2.
XX PD 08-NOV-2001.
XX PP 04-MAY-2001; 2001WO-US014646.
XX PR 04-MAY-2000; 2000US-0202028P.

(CAYL) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dunphy WG, Guo Z;
XX DR WPI; 2002-066528/09.
DR N-PSDB; AAI7202.

XX PT Novel polypeptide for regulating cell cycle progression, which is activated and phosphorylated in response to double-stranded DNA useful for diagnosing and treating cell proliferative disorder.
XX PT Claim 2: Fig 2; 75pp; English.

XX CC This sequence shows the protein kinase, Xenopus Cds1 (Xcds1) which plays a role in DNA damage checkpoint and regulating progression of cell cycle. CC The protein is characterized as phosphorylating Cdc25 or its homolog, having a molecular mass of 58 kD, 517 amino acids, SQ/TQ motifs at the CC amino terminal region, a carboxyl terminal kinase domain and an amino terminal forkhead-associated (FHA) domain. Xcds1 phosphorylates Cdc25 on Ser287 in the 14-3-3 binding site, which inhibits its activity. Xcds1 is CC activated by poly (dT)40. When Xcds1 is phosphorylated in extracts containing poly (dT)40, hyperphosphorylated Cds1 shows a five- to six-fold CC increase over background in its kinase activity towards GST-Cdc25 [254-316]-WT. The SQ/TQ motifs at the amino terminal end of Xcds1 are CC

SQ	Sequence 543 AA;	XX	New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
	Query Match 61.0%; Score 1655.5; DB 2; Length 543;	PT	
	Best Local Similarity 59.9%; Pred. No. 1.6-147;	PT	
	Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;	XX	
Qy	2 MSRDTKTESQ-----	PS	Disclosure; Page 20-23; 36pp; Japanese.
Db	1 NSRDEVAAQSHGSSACSPHGSVTSQSGSSQSGSISSTSPNNSQSSSSGTL 60	CC	The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention.
Qy	38 SSLDTVPVQDLASI-----	CC	
Db	61 SSLETSTQELYSIPEQDPEEPEPTAPWARIWALQDGPNALECNDNYWGRDKS 120	CC	
Qy	93 CDYTFDIPVNLNOTDRYTKYSKRKHFRIFQELGHGSRSVANTEDLSGNGTFTYNEKELIGKGR 152	CC	
Db	121 CBYCFDPLKRTDKRTYSKRKHFRIFREVGPKNSTAYEDHSNGTFTNTELVGKGR 180	CC	
Qy	153 LPLTNNAEIALSLPLTPNKVUFVFSIDLSDDQTYPKDFDIDKTMSPRPGSGACGEVKLAQK 212	CC	
Db	181 RPLNNNEAIALSLPLSRNPKVUFVFSIDLSDQSYPKALRDETMKSLGSGACGEVKLAQF 240	CC	
Qy	213 SVCKYAVKIKISKRKFONNTSNEHP-1SVDTEPIELUKKLDHPCTIKIEPFDSEDFYY 271	CC	
Db	241 KTCCKYAVKIKISKRKFAGGSAREADPALNVETEIILKLNHPC1IKIKNFFDAE-YYY 299	CC	
Qy	272 VIELMEGGELEFDRVNVNSTRLEPIAKLYFYOMMLAYOYLHENGVTHDLKPNENVLSSSTS 331	CC	
Db	300 VIELMEGGELEFDRVGNKVLKREATCHKLYFYOMMLAYOYLHENGVTHDLKPNENVLSSSQE 359	CC	
Qy	332 EFCCKITDFGQSKLGETSLMRTLCTGTPYLAPEVINTAGTTGYSAAVDCWSLGIVLFY 391	CC	
Db	360 EDCLIKITDFGSKLGETSLMRTLCTGTPYLAPEVLSVTAGYNRAVDWSLGIVLF 419	CC	
Qy	392 CLCGYPPESEQNSNIPKQKQIAEGKTYIAAWRNVEQAFDVLKQLLVNDPQEQLTTKQ 451	CC	
Db	420 CLSGYPPESEHRTQSVLKQDQITSGKYNFPEWAEYSEKALDLVVKCLLVDPKARFTTE 479	CC	
Qy	452 ALEHPWMLQDSMVKHHTVERLMLYCVDHTMPP--IKENNIIRKGHEDQDASTSS----C 503	CC	
Db	480 ALRHPWMLQDDMKRKFQDLSSENESTALPQVLAQFSTSRKPREGEAEGRRTKRPACV 539	CC	
Qy	504 SEIL 507	CC	
Db	540 AAVL 543	CC	
RESULT 5		RESULT 6	
ID AAM48995	Human; Chk2 phosphoenzyme inhibitor; protein; 543 AA.	ABG30701	Homo sapiens.
XX	JP2001346588-A.	ID ABG30701 standard; protein; 543 AA.	ABG30701;
XX	08-JUL-2002 (first entry)	XX ABG30701;	XX ABG30701;
XX	Human Chk2 phosphoenzyme inhibitor related protein #1.	XX ABG30701;	XX ABG30701;
XX	KW Human; Chk2 phosphoenzyme inhibitor; cytosatic.	XX ABG30701;	XX ABG30701;
OS Homo sapiens.			
XX AC AAM48995;			
XX XX			
DT 08-DEC-2001.			
XX 08-JUN-2000; 2000JP-00172273.			
XX PR 08-JUN-2000; 2000JP-00172273.			
XX XX			
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.			
XX DR WPI; 2002-145186/19.			
DR N-PSDB; AAL44750.			
PN			
07-OCT-2002 (first entry)			
XX Human checkpoint kinase 2 (CHK2) polypeptide.			
XX DE Human; checkpoint kinase 2; CHK2; enzyme; antisense therapy.			
XX KW Homo sapiens.			
OS XX			
PN XX			
WO200251858-A2.			

XX 04-JUL-2002. Qy 504 SEIL 507
 PD : :
 XX Db 540 AAVL 543
 PF XX
 PR XX
 XX 22-DEC-2000; 2000US-00746043.
 PA (ISIS-) ISIS PHARM INC.
 PA (ABBO) ABBOTT LAB.
 XX
 PI Sarthy A, Cowser LM;
 XX DR WPI; 2002-575367/61.
 DR N-PSDE; ABR88909.
 XX
 PT New antisense oligonucleotides targeted to a nucleic acid encoding
 PT checkpoint kinase 2 (CHK2), useful for treating a disease or condition
 PT associated with CHK2, or in distinguishing functions of members of a
 PT biological pathway.
 XX Disclosure: Page 87-90; 100pp; English.
 XX The invention relates to an antisense compound targeted to a nucleic acid
 CC molecule encoding human checkpoint kinase 2 (CHK2). The antisense
 CC compound specifically hybridizes with and inhibits the expression of
 CC human CHK2. The antisense compounds are useful as research reagents and
 CC diagnostics, in distinguishing between functions of various members of a
 CC biological pathway, and in the treatment of a disease or disorder, which
 CC can be treated by modulating the expression of CHK2. This sequence
 CC represents the human CHK2 protein.
 XX Sequence 543 AA;
 SQ 61.0%; Score 1655.5; DB 5; Length 543;
 Best Local Similarity 59.9%; Pred. No. 1.6e-147;
 Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
 Qy 2 M8RDTKTESQ-----QSOCTSSSSSSAP-QGYSOSSSSGTL 37
 Db 1 M5RESDVEAQSHGSSACSQPGS70TQSQSSQS06TSSSTPNSSSSSSSGTI 60
 Qy 38 S8SLDTVPVQDLASI----PDPPEIDEDIQPWGRLWALKGFLHDCLHEYYFGRDKK 92
 Db 61 SSLETVSTQDLSYSPIDQPEQPEPPTAWEARLWALQDGFAANLCEVNDNYWGRDKS 120
 Qy 93 C8YTFDIPVNLQDTRYSKRHRFLQELGGHKSRYANIEELSGNGTWNKEI1GKRT 152
 Db 121 CEYCFDEPLKETDKYRTSKKHF1FREVGPKNSTAYIEDHSGNGTFNTELYKGKR 180
 Qy 153 LPLTNNAABIALSLPPTNKFVFSQDSDQTYKIMSRPIGSAGCEVLAFOK 212
 Db 181 RPLNNNSBEIALSLSRNKFVFFPDLQSVPKARDEYIMSKTGSAGCEVLAFER 240
 Qy 213 SVCKKVAIKLISKRKFKMNTSSSNNEHP-1SVDTEIETLKKLDPCTIKIENRFDSDPYYI 271
 Db 241 KTCKKVAIKLISKRKFKAGSAREADPAPNVEETIETLKKLHNPKC1KKNFDDAED-YYI 299
 Qy 272 VIELMEGGELFDKVNSTRLRPIAKLYFYQYMLAQYHENGVIRDLKPNVLISSTS 331
 Db 300 VIELMEGGELFDKVNKNKLRKATCKLYFYQYMLAQYHENGVIRDLKPNVLISSQE 359
 Qy 332 EECCKITDFGOSKILGETSMRMLTCGTPTYLAPEVLTNTAGTGTGSSAVDWSLGTVLFV 391
 Db 360 EDLIKITDFGHSRKLGETSMRMLTCGTPTYLAPEVLTNTAGTGTGSSAVDWSLGTVLF 419
 Qy 392 CLCGYPPESEONSNIPKNOIAEGKTYIAAWRNTSEFAQFDLVKNLIVDPEQRLLTKQ 451
 Db 420 CLSGYPPESEHRTQVSLKJDQITSGSKNFIPEWTAEYSEKALDLVKECLLVDPKFARTTE 479
 Qy 452 ALERPHWQDLSMKTHTVERLLMKGVDHMP---IIRKNIRKRGHWDQDASTSS----C 503
 Db 480 ALRHPWQLQEDMKRKFQDLSLSEENESTALPQVLAQFSTSRRKPREGEAETTRKPAVC 539

RESULT 7
 ID ADL32561
 DE Human Chk2 transcript variant 1 protein SEQ ID NO:19.
 XX DT 03-JUN-2004 (First entry)
 DE Human Chk2 transcript variant 1 protein SEQ ID NO:19.
 XX
 KW detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor;
 KW cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein;
 KW progesterone receptor; cytostatic; gene therapy; squamous cell carcinoma;
 KW hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma;
 KW head and neck cancer; adenocarcinoma; squamous lung cancer;
 KW gastrointestinal cancer; renal cell cancer; bladder cancer;
 KW prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma;
 KW Chk2 transcript; variant 1.
 XX
 OS Homo sapiens.
 XX
 PN WO2004022750-A1.
 XX PD 18-MAR-2004.
 XX PP 05-SEP-2003; 2003WO-AU001164.
 XX PR 05-SEP-2002; 2002AU-00951346.
 XX PR 07-NOV-2002; 2002US-042518P.
 XX PA (GARV-) GARVAN INST MEDICAL RES.
 XX PI Watts C, Saunders D, Henderson M, Clancy J, Henshall S;
 PI Sutherland R, O'brien P;
 XX DR 2004-248472/23.
 DR N-PSDE; ADL32560.
 XX
 PT Detecting a cancer cell in a subject sample, also related to cancer
 PT treatment, comprises determining the level of nucleic acid that is
 PT linked to map position 8q22.3 of the human genome or its expression
 PT product.
 XX
 PT Claim 29; SEQ ID NO 19; 331pp; English.
 XX
 CC The present invention describes a method for detecting a cancer cell in a
 CC subject, which comprises determining the level of nucleic acid that is
 CC linked to map position 8q22.3 of the human genome or its expression
 CC product in a sample of the subject, where an elevated level of the
 CC nucleic acid or polypeptide is indicative of cancer in the subject. Also
 CC described: (1) a method for diagnosing a cancer or predicting recurrence
 CC of a cancer in a subject comprising determining the level of mRNA or
 CC nucleic acid molecule for detecting cancer cell; (2) the isolated or
 CC recombinant protein complex; (4) an antibody that binds to the protein
 CC complex; (5) a kit for detecting or producing a protein complex,
 CC comprising an EDD polypeptide or a portion of an EDD polypeptide and a
 CC second polypeptides selected from a protein having tumour suppressor
 CC activity, a protein having cell cycle modulatory activity, a protein
 CC associated with DNA repair or damage, a nuclear targeting protein, and a
 CC progesterone receptor protein or its portion, where the portion of the
 CC second polypeptide is sufficient to bind to the EDD polypeptide or the
 CC portion of an EDD polypeptide; (6) methods for isolating the protein
 CC complex; (7) a method for determining a predisposition for disease, or
 CC disease state; (8) a method for determining a modulator of the activity, or
 CC formation or stability of an isolated or recombinant protein complex; (9)
 CC a method for determining a modulator of the level of protein complex
 CC formation; (10) a method for treating a condition associated with

elevated expression of EDD protein in a cell; (11) an antisense nucleic acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and (12) a pharmaceutical composition comprising the antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such as cancer, e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human Chk2 transcript variant 1 protein, which is used in the exemplification of the present invention.

XX Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543; Best Local Similarity 59.9%; Pred. No. 1.6e-147; Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7; Qy 2 NSRDTKTESQ-----OSGTFSSSSSSAP-QYYSQSSSSGTL 37 Db 1 NSRESDEVAQOSHGSACSQPHGSVTSQSSSSQSGQISSSTSTMPNSQSSSSGTL 60 Qy 38 SSDLTYPVQDLASI----PDEPTEDEDIPOPWGRLWALGKFLNHDCLHEEYFGRDKK 92 Db 61 SSLETYVSTQELYSIPDQEPPEPTAPWRLWALQDFANLCYNDNWFGRDKS 120 Qy 93 CDYTFDIPVNLQNTDRYKTYSKRHERIFQELGHGHSRVANTEDLSGNTGTFVNKEIIGKRT 152 Db 121 CEYCFDDEPLKERTDKYRTSKCHFRFREYGPKNAYTEDHSNGTFVNTELYVGKGR 180 Qy 153 LPLTNNAIBAISLSPTPNKVYFSDLSYDQTYTPKOFIDKIMSPIGSGCAGEVYKLAQK 212 Db 181 RPLNNNSEIAISLSRKVYFFDLTVDQSYPKALRDETIMSKWLGSGCAGEVYKLAQF 240 Qy 213 SVCKKVAVKLISKRKFKMTSSNEHP--ISVDTIEILKKLDHPCIKIENFFSDBDFYY 271 Db 241 KTKCKVAKIKISKRKPAIGSREADPALNVEIEILKKLKHPCIKIKNFFDAED-YYY 299 Qy 272 VLEMMEGGELFDPRVNSTRREPIAKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSTS 331 Db 300 VLEMMEGGELFDKVNKLRKLEBATCHKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSOP 359 Qy 332 BECCIKITDQSKLIGETSLMRLTQGTPYLAPEVLNTIQTGTGQSSAVTCWSLGVLTV 391 Db 360 EDCLIKITDGFHSKLGETSLMRTLQGTPYLAPEVLVSTGTAGYNRAVTCWSLGVLTF 419 Qy 392 CLCGYBPFSEONSNIPLKQIAEGKTYIYAAWRYNVEQAFDLYRNLVYDPEORLTKO 451 Db 420 CLSGYBPFSEHRQTSLKDQTSGKINFIPEVAESEKALDVLKKLVLVPKARTFIE 479 Qy 452 ALEHPNQLDDSMKHTYERLAMYGVDTMPPP---IKKNIKTRKGHEDWDASTSS---C 503 Db 480 ALRHPNQLDDSMKHTYERLAMYGVDTMPPP---IKKNIKTRKGHEDWDASTSS---C 539 Qy 504 SEIL 507 Db 540 AAVL 543

RESULT 8

ADM72213 ID ADM72213 standard; protein; 543 AA.

XX AC ADM72213;

XX DT 17-JUN-2004 (first entry)

XX DE Human TASK108 polypeptide.

KW TASK; tumour-associated kinase; cytostatic; tumour antigen; KW cell proliferative disorder; cancer; transgenic; human.

XX OS Homo sapiens.

XX PN WO2004024064-A2.

XX PD 25-MAR-2004.

XX PP 05-SEP-2003; 2003WO-US027894.

XX PR 11-SEP-2002; 2002US-0410166P.

XX PA (GETH) GENENTECH INC.

XX PI Desauvage FJ, Wood WI, Zhang Z;

XX DR WPI: 2004-282985/26.

XX DR N-PSDB; ADM72212.

XX PR New tumor-associated kinase nucleic acids and polypeptides, useful as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing.

XX PT Claim 12; SEQ ID NO 18; 163bp; English.

XX CC The invention relates to new isolated tumour-associated kinase (TASK) nucleic acid molecules and encoded polypeptides. Cytostatic. The CC antibody, oligopeptide or organic molecule that binds to the TASK polypeptide are useful for treating a mammal, having a tumour comprising CC cells expressing the polypeptide. Antagonists of TASK are useful for CC treating or preventing a cell proliferative disorder (e.g. cancer) associated with increased expression or activity of TASK polypeptide. The CC TASK polynucleotides and polypeptides may be used as hybridization probes CC for isolating full length TASK DNA, for generating transgenic animals, in CC chromosome identification, or for tissue typing. The present sequence CC represents a human TASK polypeptide.

XX SQ Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543; Best Local Similarity 59.9%; Pred. No. 1.6e-147; Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

Qy 2 MSDLTYPVQDLASI----PDEPTEDEDIPOPWGRLWALGKFLNHDCLHEEYFGRDKK 92

Db 1 NSRDTKTESQ-----OSGTFSSSSSSAP-QYYSQSSSSGTL 37

Qy 38 SSDLTYPVQDLASI----PDEPTEDEDIPOPWGRLWALGKFLNHDCLHEEYFGRDKK 92

Db 61 SSLETYVSTQELYSIPDQEPPEPTAPWRLWALQDFANLCYNDNWFGRDKS 120

Qy 93 CDYTFDIPVNLQNTDRYKTYSKRHERIFQELGHGHSRVANTEDLSGNTGTFVNKEIIGKRT 152

Db 121 CEYCFDDEPLKERTDKYRTSKCHFRFREYGPKNAYTEDHSNGTFVNTELYVGKGR 180

Qy 153 LPLTNNAIBAISLSPTPNKVYFSDLSYDQTYTPKOFIDKIMSPIGSGCAGEVYKLAQK 212

Db 181 RPLNNNSEIAISLSRKVYFFDLTVDQSYPKALRDETIMSKWLGSGCAGEVYKLAQF 240

Qy 213 SVCKKVAVKLISKRKFKMTSSNEHP--ISVDTIEILKKLDHPCIKIENFFSDBDFYY 271

Db 241 KTKCKVAKIKISKRKPAIGSREADPALNVEIEILKKLKHPCIKIKNFFDAED-YYY 299

Qy 272 VLEMMEGGELFDPRVNSTRREPIAKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSTS 331

Db 300 VLEMMEGGELFDKVNKLRKLEBATCHKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSOP 359

Qy 332 BECCIKITDQSKLIGETSLMRLTQGTPYLAPEVLNTIQTGTGQSSAVTCWSLGVLTV 391

Db 360 EDCLIKITDGFHSKLGETSLMRTLQGTPYLAPEVLVSTGTAGYNRAVTCWSLGVLTF 419

Qy 392 CLCGYBPFSEONSNIPLKQIAEGKTYIYAAWRYNVEQAFDLYRNLVYDPEORLTKO 451

Db 420 CLSGYBPFSEHRQTSLKDQTSGKINFIPEVAESEKALDVLKKLVLVPKARTFIE 479

Qy 452 ALEHPNQLDDSMKHTYERLAMYGVDTMPPP---IKKNIKTRKGHEDWDASTSS---C 503

Db 480 ALRHPNQLDDSMKHTYERLAMYGVDTMPPP---IKKNIKTRKGHEDWDASTSS---C 539

Qy 504 SEIL 507

Db 540 AAVL 543

Qy 541 RPLNNNSEAISLSRKVYFFDLTVDQSYPKALRDETIMSKWLGSGCAGEVYKLAQF 240

Qy 542 SVCKKVAVKLISKRKFKMTSSNEHP--ISVDTIEILKKLDHPCIKIENFFSDBDFYY 271

Db 543 KTKCKVAKIKISKRKPAIGSREADPALNVEIEILKKLKHPCIKIKNFFDAED-YYY 299

Qy 544 VLEMMEGGELFDPRVNSTRREPIAKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSTS 331

Db 545 EDCLIKITDGFHSKLGETSLMRTLQGTPYLAPEVLVSTGTAGYNRAVTCWSLGVLTF 419

Qy 546 BECCIKITDQSKLIGETSLMRLTQGTPYLAPEVLNTIQTGTGQSSAVTCWSLGVLTV 391

Db 547 CLCGYBPFSEONSNIPLKQIAEGKTYIYAAWRYNVEQAFDLYRNLVYDPEORLTKO 451

Qy 548 RPLNNNSEAISLSRKVYFFDLTVDQSYPKALRDETIMSKWLGSGCAGEVYKLAQF 240

Qy 549 SVCKKVAVKLISKRKFKMTSSNEHP--ISVDTIEILKKLDHPCIKIENFFSDBDFYY 271

Db 550 KTKCKVAKIKISKRKPAIGSREADPALNVEIEILKKLKHPCIKIKNFFDAED-YYY 299

Qy 551 VLEMMEGGELFDPRVNSTRREPIAKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSTS 331

Db 552 EDCLIKITDGFHSKLGETSLMRTLQGTPYLAPEVLVSTGTAGYNRAVTCWSLGVLTF 419

Qy 553 BECCIKITDQSKLIGETSLMRLTQGTPYLAPEVLNTIQTGTGQSSAVTCWSLGVLTV 391

Db 554 CLCGYBPFSEONSNIPLKQIAEGKTYIYAAWRYNVEQAFDLYRNLVYDPEORLTKO 451

Qy 555 RPLNNNSEAISLSRKVYFFDLTVDQSYPKALRDETIMSKWLGSGCAGEVYKLAQF 240

Qy 556 SVCKKVAVKLISKRKFKMTSSNEHP--ISVDTIEILKKLDHPCIKIENFFSDBDFYY 271

Db 557 KTKCKVAKIKISKRKPAIGSREADPALNVEIEILKKLKHPCIKIKNFFDAED-YYY 299

Qy 558 VLEMMEGGELFDPRVNSTRREPIAKLYFQMLLAVQYIHLENGVTHRDLMKPEVNLLSTS 331

Db 559 EDCLIKITDGFHSKLGETSLMRTLQGTPYLAPEVLVSTGTAGYNRAVTCWSLGVLTF 419

Qy 560 CLCGYBPFSEONSNIPLKQIAEGKTYIYAAWRYNVEQAFDLYRNLVYDPEORLTKO 451

THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; osteopathic; THAP modulator; THAP synthesis modulator; human.

XX Homo sapiens.

XX WO2004055050-A2.

XX 01-JUL-2004.

XX 10-DEC-2003; 2003WO-1B006434.

XX 10-DEC-2002; 2002US-04326939P.

PR 03-JUL-2003; 2003US-0485027P.

PA (ENDO-) ENDOCUBE SAS.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Girard J., Amalric F., Roussigne M., Clouaire T;

XX WPI; 2004-525034/5.

DR N-PSDB; ADQ09233.

XX PT Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation comprises modulating the interaction of a THAP polypeptide with a nucleic acid.

XX PT Example 47; SEQ ID NO 417; 612PP; English.

XX The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/chemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy, comprising a transcription factor decoy described above; (4) a cell comprising a transcription factor element; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP/chemokine complex; (6) a vector packaging cell line comprising a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/chemokine complex; (9) methods of identifying a test compound that modulates transcription at a THAP responsive element or that modulates the transport of a THAP responsive element into the nucleus; (10) methods for reducing the symptoms associated with a condition selected from excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative diseases; symptoms associated with a condition resulting from the activity of a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation mediated by a THAP-family polypeptide in an individual; (11) a vector comprising a THAP responsive promoter operably linked to a nucleic acid encoding a detectable product; (12) a genetically engineered cell comprising the vector described above or that expresses a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation is useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

CC or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the present invention.

XX CC

XX XX

SQ Sequence 543 AA;

Query	Match	Score	Length
Qy	2 MSRDTMTEQ-----	61.0%	543;
Db	1 MSRRESVEAQOSHGSACSOHGSYTSQSCSSSSP-QsySQSSSSGSGT 37	59.9%	543;
Qy	38 SSLDTIPVQDLASI-----	59.9%	543;
Db	61 SSLETSTQELYSPIDQDQEPDQEPEPTAPWALQWALOGFANEIYDNYWGRDKS 120	59.9%	543;
Qy	93 CDYTPDIPVNLNOTDRKTYSKRHFPIFQELGHGSRSVANTEEDLSGNNTPYKEIIGKRT 152	59.9%	543;
Db	121 CEYCFDEPLKRTDCKRTYSPKHFTRFEGPKNSIAYEDHSGTFTNTELYKGK 180	59.9%	543;
Qy	153 LPLTNNAEIALSPTKVKVFSDSLSDVQDQTYPKDFTKYSIAYEDHSGTFTNTELYKGK 212	59.9%	543;
Db	181 RPLNNNSETIALSLSRNKVKVFFPDLTVDQSVYPKRLDTEYIMSKTIGSGACEVKLAFER 240	59.9%	543;
Qy	213 SVCKYAVKILSKRKFKMNTSSNHEP-1SYDTEIILKKLUDHPCTK1ENFFDSEDFYYI 271	59.9%	543;
Db	241 KTCRKVAKILSKRKFKAGSAREADPLNVEIEILKKLUNHPCITK1ENFFDSEDFYYI 299	59.9%	543;
Qy	272 VLEMMEGGLFDRVNNSTRLEPIAKLYFQMLLAQVQLHENGVTHDLKPEVNLLSTS 331	59.9%	543;
Db	300 VLEMMEGGLFDKVYGNKRKUKEATCKLYFQMLLAQVQLHENGVTHDLKPEVNLLSTS 359	59.9%	543;
Qy	332 EBCCTK1ITDFQSKKIGETSLMRTLGTPYLAPEVLNTAGTTGYSAVDQWSLGVLFV 391	59.9%	543;
Db	360 EDCLIKITDFQSKKIGETSLMRTLGTPYLAPEVLVSQTAGYNRAVDCWSLGVLFI 419	59.9%	543;
Qy	392 CLCGYPPFSEONSNIFPLKNOIAEGKTYIAAARWVNSQAFDVLVKMLVYDPEQLRTKQ 451	59.9%	543;
Db	420 CLSGYPPFSEHRTQVSLQDQITSGRNINFPEVWAESEKALDVKMLVYDPEQLRTKQ 479	59.9%	543;
Qy	452 ALEHPMLQDDSMKHTVVERIYMGVDHMTMPP---IKKNITRKGRHEDWODASTSS---C 503	59.9%	543;
Db	480 ALRHPMLQDDSMKHTVVERIYMGVDHMTMPP---IKKNITRKGRHEDWODASTSS---C 539	59.9%	543;

RESULT 11

ID AAM48996 standard; protein; 543 AA.

XX XX

XX AC AAM48996;

XX DT 08-JUL-2002 (first entry)

XX DB Human Chk2 phosphoenzyme inhibitor related protein #2.

XX XX

XX AC AAM48996;

XX OS Homo sapiens.

XX PN JP2001346588-A.

XX PD 18-DEC-2001.

XX PR 08-JUN-2000; 2000JP-00172273.

XX PR 08-JUN-2000; 2000JP-00172273.

PA	IGAKU SEIBUTSUGAKU KENKYUSHO KK.	phosphorylation; cancer; proliferative disease; cytostatic; gene therapy	
XX	XX	XX	
WPI; 2002-145186/19.	OS	Homo sapiens.	
DR; N-PSD5; AAL44751.	XX	XX	
XX	PN	W09967369-A1.	
PT	PD	29-DEC-1999.	
PT	XX	XX	
PT	PF	23-JUN-1999;	
PT	XX	99WO-JP003350.	
PT	PR	23-JUN-1998;	
PT	XX	98JP-00192467.	
PT	PA	(CHUS) CHUGAI SEIYAKU KK.	
PT	PI	Nakanishi M;	
PT	XX	XX	
PT	WPI; 2000-106292/09.	DR	
PT	DR	N-PSD5; AAL57411.	
PT	XX	XX	
PT	PT	Cell cycle regulatory factor-encoding gene for production recombinant	
PT	PT	proteins with kinase activity, used to develop drugs to treat cancers and	
PT	PT	proliferative diseases.	
PT	XX	XX	
PT	PS	Claim 1; Page 35-39; 52pp; Japanese.	
PT	XX	XX	
PT	CC	The present sequence represents the human cell cycle regulatory factor	
PT	CC	Cds1. The Cds1 nucleotide sequence can be used in gene therapy. Cds1 may	
PT	CC	be used to detect inhibitors of cell cycle regulatory factors which can	
PT	CC	be applied in the development of drugs for treating cancers and	
PT	CC	proliferative diseases. Cds1 is strongly expressed in the testis as well	
PT	CC	as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1.	
PT	XX	XX	
SQ	Sequence 543 AA;	Sequence 543 AA;	
Query Match	60.9%; Score 1651.5; DB 5; Length 543;	Query Match	60.6%; Score 1643.5; DB 3; Length 543;
Best Local Similarity	59.7%; Pred. No. 3.8e-147;	Best Local Similarity	59.6%; Pred. No. 2.2e-146;
Matches	325; Conservative	Matches	325; Conservative
Matches	75; Mismatches	75; Mismatches	104; Indels 41; Gaps 8
Qy	2 MSRTDKTQSQ-----QSQTSSSSAP-QYSQSSSSGTL 37	Qy	2 MSRTDKTQSQ-----QSQTSSSSAP-QYSQSSSSGTL 36
Db	1 MSRESDVEAQQSQSSAACQPHGSVTSQGSSSQSQTSSSSTMPNS-SQSSHSSGGT 60	Db	1 MSRESDVEAQQSQSSAACQPHGSVTSQGSSSQSQTSSSSTMPNS-SQSSHSSGGT 59
Qy	38 SSQDTVPQDLSI----PDEPEIDEDIPQWGRILWALGKGSFLNHDCLHEYYVFGDKK 92	Qy	37 LSSLDTVPQDLSI----PDEPEIDEDIPQWGRILWALGKGSFLNHDCLHEYYVFGDK 91
Db	61 SSLETVSTQVPLKXSPIDQPEPQTPAWLQWALQDQFANTLNDYWRDKS 120	Db	60 LSSLETVSTQDLSI----PDEPEIDEDIPQWGRILWALGKGSFLNHDCLHEYYVFGDK 119
Qy	93 CDYTFDIPVNLKDTQYTKYSKHFRFQBLFGHGSVNLQANIELLSQSGTFTVKEILGKRT 152	Qy	92 KCDYTFDIPVNLQNOTDVKYTSKRFHRFQBLFGHGSVNLQANIELLSQSGTFTVKEILGKGR 151
Db	121 CEYCFDDEPLKRTDKTYSKKGHRFTRPEVGPNSVIAYEDHSGNGTFTVTELVGKGR 180	Db	120 SCEYCFDDEPLKRTDKTYSKKGHRFTRPEVGPNSVIAYEDHSGNGTFTVTELVGKGR 179
Qy	153 LPLTNNNAEIALSLPLTNKVFVFSPLSDVQDQTIPKDFKYMISMRPQGAGCEVKLAFOK 212	Qy	152 TLPLTNNAEIALSLPLTNKVFVFSPLSDVQDQTIPKDFKYMISMRPQGAGCEVKLAFO 211
Db	181 RPINNSSEIALSLSRNRKVFVFFLTVDQSVPLKRDYEMISKTQGAGCEVKLAFO 240	Db	180 RRPLNNSEIALSLSRNRKVFVFFDLTVDDQSVYPAKLDVYEMISKTQGAGCEVKLAFO 239
Qy	213 SYCKKVAVKIIISKRKFKMNTSSNEHP-LSVDTIEILKLDHPCTIKIENFSDSEDFYI 271	Qy	212 KSVCKKVAVKIIISKRKFKMNTSSNEHP-LSVDTIEILKLDHPCTIKIENFSDSEDFYI 270
Db	241 1KTCKKVAVKIIISKRKFKMNTSSNEHP-LSVDTIEILKLDHPCTIKIENFSDSEDFYI 299	Db	240 RKTCKKVAVKIIISKRKFKMNTSSNEHP-LSVDTIEILKLDHPCTIKIENFSDSEDFYI 298
Qy	272 VLELMEGGBELDEEVNSTRLREPIALKYYFQMLLAVOYLHENGVIRDLKPNVLLSTS 331	Qy	271 IVLELMEGGBELDFVNSTRLREPIALKYYFQMLLAVOYLHENGVIRDLKPNVLLSTS 330
Db	300 VLELMEGGBELDFVGNKRLKEATCKLYFQMLLAVOYLHENGVIRDLKPNVLLSTS 359	Db	299 IVLELMEGGBELDFVNSTRLREPIALKYYFQMLLAVOYLHENGVIRDLKPNVLLSTS 358
Qy	332 BEECIKATDFGOSKILGETSLMRTLCGPTPLAPEVNTAGTGYSSAVDCWSLGYTLF 391	Qy	331 SSECICIKITDGFQSKILGETSLMRTLCGPTPLAPEVNTAGTGYSSAVDCWSLGYTLF 390
Db	360 EDLIKITFEGHSKILGETSLMRTLCGPTPLAPEVNTAGTGYSSAVDCWSLGYTLF 419	Db	359 BEDCLIKITDGFQSKILGETSLMRTLCGPTPLAPEVNTAGTGYSSAVDCWSLGYTLF 418
Qy	392 CLCGYPPSEQNSNPLPKNQIAEGKTYIAAARNYNSQAFDLYKLNLLVDPORLTTKQ 451	Qy	391 VCLGYPPESEONSNPLPKNQIAEGKTYIAAARNYNSQAFDLYKLNLLVDPORLTTKQ 450
Db	420 CLSGYPPSEHRTQSLKDQITSGKYNFPIETWAEVSEKALDVKKLLVDPDKARETTE 479	Db	419 ICLSGYPPSEHRTQSLKDQITSGKYNFPIETWAEVSEKALDVKKLLVDPDKARETTE 478
Qy	452 ALRHPWLDQSKMKTVERLMLGYDHTMNP-----IKNNTIRKGHENWODATSS---C 503	Qy	451 QALEHPWLDQSKMKTVERLMLGYDHTMNP-----IKNNTIRKGHENWODATSS---C 502
Db	480 ALRHPWLDQSKMKTVERLMLGYDHTMNP-----IKNNTIRKGHENWODATSS---C 539	Db	479 FAIHPWLDQSKMKTVERLMLGYDHTMNP-----IKNNTIRKGHENWODATSS---C 538
Qy	504 SEIL 507	Qy	504 SEIL 507
Db	540 AAVL 543	Db	540 AAVL 543
RESULT 12			
AYY67968;			
ID AAY67968 standard; protein, 543 AA.			
05-APR-2000 (First entry)			
Human cell cycle regulatory factor Cds1 SEQ ID NO:1.			
Human cell cycle regulatory factor Cds1; hcds1; cdc25; histone H1.			

Qy 2 M8RDTKTESQ-----QSQTSSSSSSAP-QSYSSSSSGTL 37
 Db 1 M8RSDVEAQSHGSSACSPHGSVTOQSGSSQSQGISSSTSTPNSOSSHSSGTL 60
 Qy 38 S8LDTPVQDLASI-----P8P8E8D8D10P8WGR8LWAL8GKF8LNHDCL8EYVFGRDK 92
 Db 61 SSLET8V8T8Q8L8T8P8D8Q8P8E8P8T8P8WAL8Q8D8F8N8C8V8D8N8W8F8RDK 120
 Qy 93 CDYTF8D8P8L8N8T8D8R8Y8C8K8H8F8T8Q8V8A8N8T8E8L8G8N8G8T8F8N8K8E8I8G8K8T 152
 Db 121 C8YCF8D8P8L8R8K8T8D8Y8K8H8F8T8Q8V8P8N8A8T8Y8E8D8G8N8G8T8F8N8T8E8V8G8K8R 180
 Qy 153 LP8T8N8A8I8L8P8T8N8K8V8F8S8D8Q8T8P8D8Y8K8Y8I8M8R8P8G8A8C8V8L8A8F8Q8 212
 Db 181 R8P8N8E8I8L8S8R8N8V8F8V8F8D8L8T8D8Q8T8P8K8L8R8D8Y8E8M8K8T8G8A8G8E8V8L8A8F8R 240
 Qy 213 SV8CK8V8K8I8S8K8F8K8N8T8S8N8H8P8-18V8D8T8E8I8L8K8D8H8P8C8I8K8I8E8N8F8D8E8F8Y8I 271
 Db 241 K8T8CK8V8K8I8S8K8F8K8A8G8S8A8R8A8D8P8A8N8V8E8T8I8L8K8N8H8P8C8I8K8I8N8F8D8A8E8D8-Y8I 299
 Qy 272 V8E8L8M8G8E8L8D8V8N8T8L8R8P8I8K8Y8F8Q8M8L8A8Q8Y8L8H8N8V8I8R8D8L8P8V8N8L8S8T8 331
 Db 300 V8E8L8M8G8E8L8D8F8K8V8G8N8K8L8E8T8C8K8I8F8Q8M8L8A8Q8------ 336
 Qy 332 E8C8I8K8T8D8G8S8K8I8E8T8L8C8T8P8I8L8A8P8V8N8T8A8P8I8V8L8A8P8V8I8G8V8L8F8 391
 Db 337 -----18D8F8G8S8K8I8E8T8L8C8T8P8I8L8A8P8V8N8T8A8P8I8V8L8A8P8V8I8G8V8L8F8 390
 Qy 392 C8L8G8Y8P8F8E8Q8N8I8P8K8I8Q8A8G8K8Y8I8A8W8R8V8S8E8Q8F8D8L8V8N8L8V8D8P8Q8L8T8K8 451
 Db 391 C8L8G8Y8P8F8E8R8T8Q8S8L8K8Q8I8T8G8K8N8F8I8P8W8A8E8V8A8D8L8V8K8L8V8D8P8K8F8T8E8 450
 Qy 452 A8E8H8P8W8Q8D8M8K8H8T8V8E8R8L8Y8G8V8D8H8M8P8---I8K8N8I8R8G8H8W8D8A8S8-----C 503
 Db 451 A8R8H8P8W8Q8D8M8K8F8Q8L8S8E8N8E8T8A8P8V8L8Q8V8A8E8G8A8E8T8K8P8A8V8C 510
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 Db 511 A8V8L 514

Search completed: July 7, 2005, 12:59:10
 Job time : 166 secs

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4	1655.5	61.0	543	Sequence 417, Appli
5	1655.5	61.0	543	Sequence 2, Appli
6	1644.5	60.6	545	Sequence 6, Appli
7	1643.5	60.6	543	Sequence 1, Appli
8	1049	55.3	514	Sequence 9, Appli
9	1096.5	40.4	326	Sequence 9, Appli
10	1096.5	40.4	327	Sequence 8, Appli
11	836.5	30.8	459	Sequence 9, Appli

Copyright (c) 1993 - 2005 Compugen Ltd.	Gencore version 5.1.6	Sequence 1578, Appli
OM protein - protein search, using SW model		Sequence 4, Appli
Perfect score: 2712	1 MMSRDTKTESQQSQQTSSSS.....ASTSSCSELPTSAEKRARR 517	Sequence 4, Appli
Sequence: 1 MMSRDTKTESQQSQQTSSSS.....ASTSSCSELPTSAEKRARR 517		Sequence 10, Appli
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Scoring table: BLOSUM62		Sequence 2, Appli
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Gapext 0.5		Sequence 2, Appli
Perfect score: 2712		Sequence 2, Appli
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Total number of hits satisfying chosen parameters:		Sequence 7, Appli
Post-processing: Minimum Match 10.0%		Sequence 4, Appli
Minimum DB seq length: 0		Sequence 4, Appli
Maximum DB seq length: 2000000000		Sequence 10, Appli
Post-processing: Maximum Match 10.0%		Sequence 10, Appli
Listing first 45 summaries		Sequence 10, Appli
Database :	Published Applications AA:*	RESULT 1
	1: /cgn2_5/ptodata/1/pubpa/US07_PUBCOMB.pep:*	US-09-849-617-2
	2: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*	; Sequence 2, Application US/09849617
	3: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*	; Publication No. US20080086322A1
	4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB.pep:*	; GENERAL INFORMATION:
	5: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*	; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
	6: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*	; APPLICANT: GUO, Zijian
	7: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep:*	; APPLICANT: DUNPHY, William
	8: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep:*	; TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
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	10: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep:*	; CURRENT APPLICATION NUMBER: US/09/849,617
	11: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep:*	; CURRENT FILING DATE: 2001-09-17
	12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUBCOMB.pep:*	; PRIORITY APPLICATION NUMBER: US 60/202,028
	13: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep:*	; PRIORITY FILING DATE: 2000-05-04
	14: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep:*	; NUMBER OF SEQ ID NOS: 14
	15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep:*	; SOFTWARE: Patentin version 3.0
	16: /cgn2_6/ptodata/1/pubpa/US10E_PUBCOMB.pep:*	; SEQ ID NO: 2
	17: /cgn2_6/ptodata/1/pubpa/US10F_PUBCOMB.pep:*	; TYPE: PRT
	18: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUBCOMB.pep:*	; ORGANISM: Xenopus laevis
	19: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.pep:*	; LENGTH: 517
	20: /cgn2_6/ptodata/1/pubpa/US11_NEW_PUBCOMB.pep:*	US-09-849-617-2
	21: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUBCOMB.pep:*	
	22: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match	100.0%	Score 2712; DB 9;
Best Local Similarity	100.0%	Pred. No. 3.5e-193; Pred. No. 3.5e-193;
Matches 517; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSRDTKTESQQSQQTSSSSAPSSGYSQSSSSGTSSSLDTVPQLASIPEDPEIDED 60		
Dy 1 MMSRDTKTESQQSQQTSSSSAPSSGYSQSSSSGTSSSLDTVPQLASIPEDPEIDED 60		
Qy 61 IPQPWGRWLWALKGKFNHDCLHEEYFGDRKCDYFDIPVNLNOTRYKTYSKRHRIFQ 120		
Dy 61 IPQPWGRWLWALKGKFNHDCLHEEYFGDRKCDYFDIPVNLNOTRYKTYSKRHRIFQ 120		

Qy 272 VLELMEGGLEFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHENGVIHDLKPENVLSSSTS 331
 Db 300 VLELMEGGLEFDRVGNKRLKEATCKLYFYQMLLAVOYLHENGVIHDLKPENVLSSQE 359

Qy 332 BECCIKITDFGOSKILGETSLMRTLCGTPTYLAPEVINTAGTGYSSAVDCWSLGTLFV 391
 Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLSVGPAGYNRAVDWSLGTLF 419

Qy 392 CICGYPSEQNSNPLKQIARGKTYIAAWRNYSQAFDLYKNLVVDPEQRLLTKQ 451
 Db 420 CLSGYPSEEHRTQVSLKDQITSGKKNFPEWAEVSEKALDLVKKLUVVDPKARFTEE 479

Qy 452 ALRHPWLODDSMKHTVERBLMVGVDHTMPP--IKNNIIRKGHEWDQDASTSS---C 503
 Db 480 ALRHPWLODDMKRKFDQDLSEENESTALPOVLAQDSTSRCRPREGEAEGATTKRPAVC 539

Qy 504 SEIL 507
 Db 540 AAVL 543

RESULT 5
 US-10-820-583A-2
 Sequence 2, Application US/10820583A
 Publication No. US20040242461A1
 GENERAL INFORMATION:
 APPLICANT: Schneider, Michael
 APPLICANT: Oh, Hidemasa
 APPLICANT: Modulators of Telomere Stability
 FILE REFERENCE: HO-P02673US1
 CURRENT APPLICATION NUMBER: US/10/820,583A
 PRIORITY FILING DATE: 2004-04-08
 PRIORITY APPLICATION NUMBER: US 60/461,095
 PRIORITY FILING DATE: 2003-04-08
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 543
 TYPE: PRT
 ORGANISM: Human
 US-10-820-583A-2

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
 Best Local Similarity 59.9%; Prod. No. 1.5e-114; Pred. No. 1.5e-114;
 Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

Qy 2 MSRDTKTESO-----QSGTSSSSSSAP-QSISQSSSGT 37
 Db 1 MSRDSVDEAQSHGSSACSQPHGSVTQSGSSSQGSSSSTSPNSSSSHSSGGTL 60

Qy 38 SSLLDTVPQDLSI-----PDPPEIDEDIPDPWGRWLALGKFLNHDCLHBEVPGDRDK 92
 Db 61 SSLLDTVPQDLSI-----PDPPEIDEDIPDPWGRWLALGKFLNHDCLHBEVPGDRDK 120

Qy 93 CDYTFDIPLNQFDRYKTSKRHRIFOLGLGHSHSRVANTEDSLNGNTFVNKEIIGKRT 152
 Db 121 CEYCFDPLKRTDKRTYSKHKRFLREVCPKNSTAYTEHSGNTFVNTELVGKGR 180

Qy 153 LPLTNNAAEIALSPTNKKPRTNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 212
 Db 181 RPLNNNSEIALSLSRKVVFDDTQDQSKYMLPQKARDEYIMSKTGSACEVKLAFER 240

Qy 213 SVCKKVAVKLISKRKFKRNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 271
 Db 241 KTCKVAVKLISKRKFKRNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 299

Qy 272 VLELMEGGLEFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHENGVIHDLKPENVLSSSTS 331
 Db 300 VLELMEGGLEFDKVGNKRLKEATCKLYFYQMLLAVOYLHENGVIHDLKPENVLSSQE 359

Qy 332 BECCIKITDFGOSKILGETSLMRTLCGTPTYLAPEVINTAGTGYSSAVDCWSLGTLFV 391
 Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLSVGPAGYNRAVDWSLGTLF 419

Qy 392 CLCGYPSEQNSNPLKQIARGKTYIAAWRNYSQAFDLYKNLVVDPEQRLLTKQ 451
 Db 420 CLSGYPSEEHRTQVSLKDQITSGKKNFPEWAEVSEKALDLVKKLUVVDPKARFTEE 479

Qy 452 ALRHPWLODDSMKHTVERBLMVGVDHTMPP--IKNNIIRKGHEWDQDASTSS---C 503
 Db 480 ALRHPWLODDMKRKFDQDLSEENESTALPOVLAQDSTSRCRPREGEAEGATTKRPAVC 539

Qy 504 SEIL 507
 Db 540 AAVL 543

RESULT 4
 US-10-733-878-417
 Sequence 417, Application US/10733878
 GENERAL INFORMATION:
 APPLICANT: Jean-Philippe Girard
 APPLICANT: Francois Amaïric
 APPLICANT: Myriam Roussigne
 APPLICANT: Thomas Clouaire
 TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL PROLIFERATION AND CELL DIFFERENTIATION
 FILE REFERENCE: BIOANK 012A
 CURRENT APPLICATION NUMBER: US/10/733,878
 CURRENT FILING DATE: 2003-12-10
 PRIORITY NUMBER: 60/432699
 PRIORITY FILING DATE: 2002-12-10
 PRIORITY APPLICATION NUMBER: 60/485027
 PRIORITY NUMBER: 60/432699
 PRIORITY FILING DATE: 2003-07-03
 NUMBER OF SEQ ID NOS: 535
 SOFTWARE: Pastaseq for Windows Version 4.0
 SEQ ID NO: 417
 LENGTH: 543
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-733-878-417

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
 Best Local Similarity 59.9%; Prod. No. 1.5e-114; Pred. No. 1.5e-114;
 Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

Qy 2 MSRDTKTESO-----QSGTSSSSSSAP-QSISQSSSGT 37
 Db 1 MSRDSVDEAQSHGSSACSQPHGSVTQSGSSSQGSSSSTSPNSSSSHSSGGTL 60

Qy 38 SSLLDTVPQDLSI-----PDPPEIDEDIPDPWGRWLALGKFLNHDCLHBEVPGDRDK 92
 Db 61 SSLLDTVPQDLSI-----PDPPEIDEDIPDPWGRWLALGKFLNHDCLHBEVPGDRDK 120

Qy 93 CDYTFDIPLNQFDRYKTSKRHRIFOLGLGHSHSRVANTEDSLNGNTFVNKEIIGKRT 152
 Db 121 CEYCFDPLKRTDKRTYSKHKRFLREVCPKNSTAYTEHSGNTFVNTELVGKGR 180

Qy 153 LPLTNNAAEIALSPTNKKPRTNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 212
 Db 181 RPLNNNSEIALSLSRKVVFDDTQDQSKYMLPQKARDEYIMSKTGSACEVKLAFER 240

Qy 213 SVCKKVAVKLISKRKFKRNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 271
 Db 241 KTCKVAVKLISKRKFKRNTSSNEHP-1SYDTEIELKKLDPCKIENPFDSEDFYYI 299

Qy 272 VLELMEGGLEFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHENGVIHDLKPENVLSSSTS 331
 Db 300 VLELMEGGLEFDKVGNKRLKEATCKLYFYQMLLAVOYLHENGVIHDLKPENVLSSQE 359

Qy 332 BECCIKITDFGOSKILGETSLMRTLCGTPTYLAPEVINTAGTGYSSAVDCWSLGTLFV 391
 Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLSVGPAGYNRAVDWSLGTLF 419

392 CLCGYPFPSEONSNIPLKNOIAEGKTYIAAWRNVSQAFDLVKNLIVVDPERRQLTTKQ 451
 420 CLSGYPFPSEARTQVSUKDQTSKYNFPEWAEYSEKALDLVCKLIVVDPKARFTTE 479

RESULT 7
 ; Sequence 1, Application US/09740627
 ; Patent No. US2003012964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nakaniishi, Makoto
 ; TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
 ; FILE REFERENCE: 06501-071001
 ; CURRENT APPLICATION NUMBER: US/09/740,627
 ; PRIOR APPLICATION NUMBER: PCT/JP99/03350
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: JP 10/192467
 ; PRIOR FILING DATE: 1998-06-23
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 543
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: US-10-142-356-6

CURRENT APPLICATION NUMBER: US/10/142,356
 ; Sequence 6, Application US/10142356
 ; Publication No. US20030136183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boylan, John F.
 ; APPLICANT: Bowers, Alex J.
 ; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
 ; FILE REFERENCE: 0101737177A
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 60/290,276
 ; PRIOR FILING DATE: 2001-05-10
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-142-356-6

RESULT 6
 ; Sequence 6, Application US/10142356
 ; Publication No. US20030136183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boylan, John F.
 ; APPLICANT: Bowers, Alex J.
 ; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
 ; FILE REFERENCE: 0101737177A
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 60/290,276
 ; PRIOR FILING DATE: 2001-05-10
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-142-356-6

Query Match 60.6%; Score 1643.5; DB 9; Length 543;
 Best Local Similarity 59.6%; Pred. No. 1.2e-113;
 Matches 325; Conservative 75; Mismatches 104; Indels 41; Gaps 8;

Qy 2 MSLDTKTESQ-----
 Db 1 MSLRESVEAQOSHGSACSPHGSVYQSGSSSQCGISSSSTMPNS-SQSSHSSGT 59

Qy 37 LSSLDDTPVPQDPLASI-----
 Db 60 ISSLSETVSTQDLYSFLPQDPEDQPEEEPPAPMRLWALQDFANLCYNDNYWGRDK 91

Qy 92 KCDYTPDIPVLNQNTDRYKTYSKRHFRIPELGHGSRSRVANTEDLSGNGTFTNKEITGKGR 151
 Db 120 SCEYCDPEPLKRITGRYKTYSKRHFIREVGPKNSYIAVEDHSGNGTFTNTELGKGR 179

Qy 152 TLPLTNAEIALSPLTNPKVFWPSDLSVDDQTIYPKDFIDKYMRSRIGSGACGEYVLAFO 211
 Db 180 RRPLANNSEALSLSRNKVFVFDLTDQSVPKALRDEYIMSKMLGSGACGEYVLAFO 239

Qy 212 KSVCKRVAKLISKRFKFRNTSNBHP-ISVDTDEILKLLDHPCTIKENFFDSEDFYY 270
 Db 240 RKTCKRVAKLISKRFKFRNTSNBHP-ISVDTDEILKLLDHPCTIKENFFDSEDFYY 298

Qy 271 IVLELMEGGELFDRLVNSTLREPIAKLYFYQMLIAQVYLHENGTHRDLKPKENVLSSST 330
 Db 299 IVLELMEGGELFDLKVGNKRLKEATCKLYFYQMLIAQVYLHENGTHRDLKPKENVLSSST 358

Qy 331 SEECC1KITDQGSKLKGLETSLMRTLCGTPTYLAPFVLNTAGTTGYSAYDCWSLGVLF 390
 Db 359 EEDCL1KITDQGSKLKGLETSLMRTLCGTPTYLAPFVLVSYGTAQYRNADVDCWSLGVLF 418

Qy 391 VCLGYPFPSEQNSNPLKNOIAEGKTYIAAWRNVSQAFDLVKNLIVVDPERRQLTTK 450
 Db 419 ICLGYPFPSEHRTQSLQDQITSQYCFIPEWAEISCTLDLVKKLUVDPKARFTTE 478

Qy 451 QALEBHPWLQDDSMKETVERLMYGDHTMPPP---IKKNTNIRKGHWQDASTSS----- 502

Db 479 BALRHPWLQDDMKRKFQDLUSEENSTALPQVLAOPSTSRRPREGAEAGTTRPAV 538

RESULT 8
 ; Sequence 8, Application US/10820583A
 ; Publication No. US20040242461A1

US-10-820-583A-3

Qy 476 HTMPPPI-KKNIIRKGHWED-QDASTS----CSBIL 507
 ; Sequence 3, Application US/10820583A
 ; Publication No. US20040242461A1

Db 503 CSEIL 507
 Db 539 CAAVL 543

Qy 416 KYTIAAWRNVSQAFDLVKNLIVVDPERRQLTTKONLQDSSMKTVERLMYGD 475
 Db 447 KYNLIPETWTDSEKALDVLVKLUVDPKARLTTEAHLSPWLMKKEQDLYVEK 506

Qy 327 CKLYFYQMLAVQLHENGTHRDLKPKENVLSSQEDCLXKIDTSQSKLKGLETSLMRT 386

Qy 356 LCQTPTYLAPEVINTAGTTGYSAYDCWSLGVLFVCLGYPFPSEHKTQSLQDQITSQ 415
 Db 387 LCQTPTYLAPEVILSNTAGTTGYSAYDCWSLGVLFICLGSYPPFSEHKTQSLQDQITSQ 446

Qy 416 KYTIAAWRNVSQAFDLVKNLIVVDPERRQLTTKONLQDSSMKTVERLMYGD 475
 Db 447 KYNLIPETWTDSEKALDVLVKLUVDPKARLTTEAHLSPWLMKKEQDLYVEK 506

Qy 507 NLVPLPLAPAQTSGQKRELEDAEASSKRLAVCKAVL 545

GENERAL INFORMATION:

APPLICANT: Schneider, Michael
APPLICANT: Oh, Hidemasa
TITLE OF INVENTION: Modulators of Telomere Stability

FILE REFERENCE: HO-P02673US1

CURRENT APPLICATION NUMBER: US 10/820,583A
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US 60/461,095
PRIOR FILING DATE: 2003-04-08

NUMBER OF SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 514
ORGANISM: Human
US-10-820-583A-3

Query Match 55.3%; Score 1499; DB 16; Length 514;
Best Local Similarity 55.5%; Pred. No. 6e-103; Indels 68; Gaps 8;
Matches 302; Conservative 72; Mismatches 102; Indels 68; Gaps 8;

Qy 2 NSRDTKTESQ-----Q-----QSGTSSSSSSSSAP-QS-SQSSSSGTL 37
Db 1 MSRESDVEAQSSQSHGSSACSQPHGSVTSQGSSSQGSSSSTSPNSOSSSSGTL 60
Qy 38 SSDLTTPVQDLSI-----PDPDPEIDEDIPQWGRGLWALKGKFLNHDCLREYVGRDKK 92
Db 61 SSLETVTQELYSIPEQDPEQEPETPAFWARLWALQDFANLBCVNDNYWFRDKS 120
Qy 93 CDYTFDIPVNLNQDTRKTYSKRHRFRQELGHGHSRVANIEPDLSGNGTTPNKEITCKGRT 152
Db 121 CEYCFDPSPLKETDKYRTYSKCHFRFREVGPKNSTAYIEDHSNGNTTPNTELVSKGKR 180
Qy 153 LPITNNAEALSPITPLKQKQFQDQDQTYPKDFDQKQFQDQDQTYPKDFDQKQFQ 212
Db 181 RPUNNNSEITALSLSRNKVFVFPDLTVDQSVTPKALRDEYMSKTLGSGAGEVKLAFER 240
Qy 213 SVCKVAVKIIISKRKEFMTSSNEHP-1SVDTDEIELKKLDHPCILKIKENFDSDFYYI 271
Db 241 KTCKVAVKIIISKRKEFAGSAREADPAINVETEIELKKLNHPCITKIKNFDAAED-YYI 299
Qy 272 VLELMEGCBELFDRVYNSTRLEPIAKYFYQMLAVQYLHENGVIRDLKPENVLSTS 331
Db 300 VLELMEGCBELFDRVYNSTRLEPIAKYFYQMLAVQ-----336
Qy 332 EECIKITDFGOSKILGTSIARLTCGTPYLAPEVNTAGTGYSSAVIDWSLGVLFV 391
Db 337 -----ITDGFHSKILGETSILMRLCGTPYLAPEVLSVGTAGYRNADWSLGVLFV 390
Qy 392 CLCGYPPESEONSNIPLKQTAEGKTYIIAAWRNVEQAFDLVKNLLVDPPEQRLTTKQ 451
Db 391 CLSGYPPESEHRTQVSLKDQITSGKNTFPEVWAEEVKALDLVKLVLVDPKARFTE 450
Qy 452 ALHPWLODDSMKHTVERLMLYGVDHMPP--IKANIRKRGHEDQDASTSS---C 503
Db 451 ALHPWLOQEDMKRFQDLUSEENESTALPOVLAOPSTSRSKPREGEAEGETTKPACV 510
Qy 504 SEIL 507
Db 511 AAVL 514

RESULT 9
US-10-881-124A-9
Sequence 9 Application US/10881124A
Publication No. US20050112746A1
GENERAL INFORMATION:
APPLICANT: Structural Genomix, Inc.
APPLICANT: Antonysamy, Stephen S.
APPLICANT: Handle, Jorg
APPLICANT: Louie, Gordon V.

APPLICANT: Antonysamy, Stephen S.
APPLICANT: Handle, Jorg
APPLICANT: Louie, Gordon V.
TITLE OF INVENTION: Crystals and structures of Protein Kinase CHK2
FILE REFERENCE: 022132-001210US

CURRENT APPLICATION NUMBER: US 10/881,124A
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/484,389
PRIOR FILING DATE: 2003-07-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 9
LENGTH: 326
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-881-124A-9

Query Match 40.4%; Score 1096.5; DB 17; Length 326;
Best Local Similarity 64.8%; Pred. No. 3e-73; Mismatches 66; Indels 5; Gaps 3;
Matches 210; Conservative 43; Mismatches 66; Indels 5; Gaps 3;

Qy 180 DQTIYKDFDIDKYIMSRPISSGACCEVKLAFQKSVKVAVKIIISKRKFQMTNTSSNEHP-238
Db 3 DQSVYKEKALRDEYINSTKLGGACSEVKLAFERKTKVVAIKLISKRKFAIGSAREADPA 62
Qy 239 ISVDTTEIELRKLDHICIIKIENFDSDFYYIYVLELMEGELDFEVNNSTRLREPJAKL 298
Db 63 LNVETEIELLKLNHCECIIKIKNFFDAED-YVYVLELMEGELDFVGNKRLKEATCKL 121
Qy 299 YFYQMLAVQYLHENGVIRDLKPENVLSSSTSEECIKITDFGOSKILGETSLMRLTLCG 358
Db 122 YFYQMLAVQYLHENGVIRDLKPENVLSSQEEDEDLIKITDFGHSKILGETSLMRLTLCG 181
Qy 359 TPTYLAPEVNTAGTGYSSAVDWSLGVLFVLCUGYPPESEONSNIPLKQIAEGKTY 418
Db 182 DPTYLAPEVPLVSVGTPAGYRNADWSLGVLFICLUSGYPPESEHRTQVSLKDQITSGKVN 241
Qy 419 YTAAAATRNVSQAFDLYKNNLUVDPQRLITKQALHPWLODDSMHRTVERLMLYGVDHMT 478
Db 242 FIPPEVVAEVSEKALDVKLVLVDPKARFTEEARLHPWLOQEDMKRFQDLUSEENEST 301
RESULT 10
US-10-881-124A-8
Sequence 8 Application US/10881124A
Publication No. US20050112746A1
GENERAL INFORMATION:
APPLICANT: Structural Genomix, Inc.
APPLICANT: Handle, Jorg
APPLICANT: Louie, Gordon V.
FILE REFERENCE: 022132-001210US
CURRENT APPLICATION NUMBER: US 10/881,124A
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/484,389
PRIOR FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/509,781
PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
LENGTH: 327
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Predicted sequence of CHK2D expressed protein
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: serine at position 1 is phosphorylated

US-10-881-124A-8

Query Match Score 1096 5; DB 17; Length 327;
Best Local Similarity 40.4%; Pred. No. 3e-73; Score 1096 5; DB 17; Length 327;
Matches 210; Conservation: 43; Mismatches 66; Indels 5; Gaps 3;

Qy 180 DOTIYKDFDIDKYMISRPISGACGKVLAQPSVCKCKVAKVIIISKRKPFQNTSSNEHP- 238
Db 3 DQSVYPAKLDPEYIMSKTLGSACGKVLAERKTCCKVAKVIIISKRKPFQNTSSNEHP- 238

Qy 239 ISVDTETBILKLDHPECIICLKENFFDSEDFYYIVIYLMEGBELFDKVGNKRLKATCKL 298
Db 63 LAVETEETIILKLNHPCIIKTKNFFDAD-YIVIYLMEGBELFDKVGNKRLKATCKL 121

Qy 299 YFYQMLLAQVYLHENGYTHRDLPKENVYLLSSECCIKLTDQSKILLGETSLMRTLCG 358
Db 122 YFYQMLLAQVYLHENGYTHRDLPKENVYLLSSECCIKLTDQSKILLGETSLMRTLCG 181

Qy 359 TPTYLAPLEVNTAGTCYSSAVDCMSLGLVLFVCLCGYPSESEQNSNIPKQIAEGRY 418
Db 182 DPTYLAPBVLVSYGTVNRAVDCWSLGVLFVCLCGYPSESEQNSNIPKQIAEGRY 241

Qy 419 YTAAGAWNNSVSEAFDLYVNLVYDPEQRLTQKALHPWLODDSMKHTVERLHYGDHTM 478
Db 242 PIPEVAEVESEKALDLYVNLVYDPAKFTTEAHLHPWLODDSMKHTVERLHYGDHTM 301

Qy 479 PPP--IKKNIKTRKGHEWDDAS 499
Db 302 ALPQVLAQPSTSRSKRPRGEAEGA 325

RESULT 11
US-09-740-627-9
Sequence 9, Application US/09740627
Patent No. US2001296A1
GENERAL INFORMATION:
APPLICANT: Nakaniishi, Makoto
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/JP99/03350
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: JP 10/192467
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 9
LENGTH: 459
ORGANISM: Drosophila melanogaster

US-09-740-627-9

Query Match Score 30.8%; Pred. No. 1e-53; Score 30.8%; Pred. No. 37.8%; Pred. No. 1e-53; Length 459;
Best Local Similarity 37.8%; Mismatches 89; Indels 53; Gaps 11; Matches 188; Conservation: 89; Mismatches 167; Indels 53; Gaps 11;

Qy 2 MSRDTKTESQSGQTSSSSSSAPQSYSSQSSSGTSSLIPTVYDPLASITPDEPDEDI 61
Db 1 MARDT---QSGQGT-----OSQASNINTQVESQPMEXIV----- 31

Qy 62 PQPGWRLWALGKGFLNHDCLBEYFGDRKCKDYTE---DPP--VNLQTRDRYKTYSKRHP 116
Db 32 ---WGRLYGKNTKIKSUDLNNDEFTAGREANDLILNLDPEKILTR-----1SKVHP 82

Qy 117 RIFQELGHRGHISVANTEDLSNGNTGTYKTEIGKGRTLPLTNAAETALSLPINKVVFSDL 176
Db 83 -IKRANCELTINPVYIOPDLSRNGNTGTYKTEIGKGRTLPLTNAAETALSLPINKVVFSDL 141

Qy 177 SYDDQTYTYPDKDIDKYMISRPISGACGKVLAQPSVCKCKVAKVIIISKRKPFQNTSSNEHP- 235
Db 142 SPNESTGSLPEEINKTYTVNRKLGSGAYGLVRLVYDTRTCQOFAMKVNMLSGARPSTN 201

Qy 236 -EHPISSVDTBIEILKLDHPECIICLKENFFDSEDFYYIVIYLMEGGELFDRVVNSTRLREP 294
Db 202 FSDPDRVLAERAKIMONLSPRCVVMRHDIVKDPDSVYVLEFMRSGDILLRITISNKULISED 261

Qy 295 IAKLYFYQMLLAQVYLHENGYTHRDLPKENVYLLSSECCIKLTDQSKILLGETSLMR 354
Db 262 ISKLYFYQMLLAQVYLHENGYTHRDLPKENVYLLSSECCIKLTDQSKILLGETSLMR 321

Qy 355 TLCGTPTYLAPLEVNTAGTCYSSAVDCMSLGLVLFVCLCGYPSESEQNSNIPKQIAE 414
Db 322 TLCGTPLYLAPLEVNTAGTCYSSAVDCMSLGLVLFVCLCGYPSESEQNSNIPKQIAE 380

Qy 415 GKTYTIAAMRNVSSEQAFDLVNLIVDPEQRLTQKALEHPWLODSMKHTVERLML--- 471
Db 381 GRFAYGHPSKSVSQRKULINQMLVQKARBLMKLD 440

Qy 472 --YGVDTHTMPPPIKNN 485
Db 441 GMEIEBENFLEPEPTGRS 457

RESULT 12
US-10-369-493-1578
Sequence 1578, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIORITY FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/3360,039
NUMBER OF SEQ ID NOS: 4374
SEQ ID NO: 1578
LENGTH: 513
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae

US-10-369-493-1578

Query Match Score 22.9%; Score 621; DB 15; Length 513;
Best Local Similarity 32.1%; Pred. No. 1e-37; Mismatches 152; Indels 90; Gaps 12; Matches 149;

Qy 88 GRDKKCDYTFDIPUNQTDYKTYSKRHFRIQELGHGHSRVAINTERLDSNGNTFYNEKII 147
Db 59 GRSRSCDV-----ILSEPD-1STPFAEFLHQMDVNFQRLNINVTDKSRNGTFNGNRL 112

Qy 148 GKGRTLPLTNAAETALSLPINKVVF-----SDLSVDDQTI----- 183
Db 172 SATSSONATSAATKLNKTRPVSFQDQYKGEAGHYALVKEAKNKTGQQAVKIF 231

Qy 184 -----YPKDPTDQYKTMRSRPIGSAGCEVKLAQKSVKKKVAVKII 223
Db 113 VK-KDYLKNGDRIVFGKCSPLFKYASSSTSDBNDDEKVSSESRSYKNDDEVPKKPQI 171

Qy 224 SKRK--FRONTSSNEHPISYVDTLEILKLDHPQIK---TENFFDSEDFYYVYLEL 275
Db 232 HAQONDQDKNQKQFNE-----ETNLLARVQHNPVNLLDSFVEPIKSQIOKYLVLEK 284

Qy 276 MEGGEFDRVVNSTRLREPIAKLYYYQMLLAVQYHENGYTHRDLPKENVYLLSSEEE-- 333
Db 285 IDDGELFIERVTKTCRQDSKALPKQQLTGLKYLHEQNIHHRDIKPENILNTRENP 344

Qy 334 -----CCIKITDGFQSKILGTSLMLRTCGTPYLAPEVINTAGTYGSSA 379
Db 345 SQVQLQGPWDEDEDIOVQKIADEGLAKFTGENQFTNTLCGTPSYVAPEVLT--KKGYTSK 401

Qy	380	VDCTWSLGVLFVCLGPPFPSEONSINPLKQIAEGKTYIAAWRNVSSEQAFDVLKVNLL	439
Db	402	VDLWSAGVLYVCLGPPFPSDLQGPPSLKEQIQLQAKYFSPYDVKDSSVLHJSNL	461
Qy	440	WDPEFQLRTTKOALEHPWQLD-----DSMKHTVVERLXMGYDHTMP	479
Db	462	VLPNFDERYNIDEALNHPWENDIOQOSSVSLERLQRQI-TDNKIP	504
RESULT 13			
US-09-733-388-4			
; Sequence 4, Application US/09733388			
; Publication No. US2003006495A1			
; GENERAL INFORMATION:			
; APPLICANT: Donoho, Greg			
; APPLICANT: Scoville, John			
; APPLICANT: Turner, C. Alexander Jr.			
; APPLICANT: Friedrich, Glenn			
; APPLICANT: Zambrowicz, Brian			
; APPLICANT: Abuin, Alejandro			
; APPLICANT: Sands, Arthur T.			
; TITLE OF INVENTION: No. 6620698el Human Kinase Proteins and			
; TITLE OF INVENTION: Polynucleotides Encoding the Same			
; FILE REFERENCE: LEX-0103 USA			
; CURRENT APPLICATION NUMBER: US/09/733,388			
; CURRENT FILING DATE: 2000-12-07			
; PRIORITY APPLICATION NUMBER: US 60/169,428			
; PRIORITY FILING DATE: 1999-12-07			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: Fasle SEQ For Windows Version 4.0			
; SEQ ID NO: 4			
; LENGTH: 356			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-733-388-4			
Query Match Score 603; DB 10; Length 356;			
Best Local Similarity 38.1%; Pred. No. 1.7e-36; Gaps 6;			
Matches 128; Conservative 62; Mismatches 106; Indels 40;			
Qy	198	IGSGAGCEVKLAQKSVCKKAVAKIISKRKFKNNTSSNEHPIVSUTEIEILKKLJDHPCII	257
Db	29	LQGTCFAFSEVVLAAEKAATGKFLAVKCIPKALKGKES-----SINEIAVLRKICHENY	82
Qy	258	KIENPFDSDPFYIVLMEGGELFDRVNSTRLEPIAKLYFQMLAVQLHENGVIIH	317
Db	83	ALEDIYEESENPHLYLVMQLVSGGELFDRIIVEKGFTYEKDASTLIRQVLDAYVYLHMGIVH	142
Qy	318	RDLIKPENLSSSTSECCCIKITDQFQSKILGETSMRMLCTGPTYLAPEVLTNTACTGTGYS	377
Db	143	RDLIKPENLSSYQSOBEESKIMSDFGLSKMEGKDDMSTAGTPGVAPEV-----AQKPY5	199
Qy	378	SAYDWSLGSVLFVCLGPPFPSEONSINPLKQIAEGKTYIAAWRNVSQADLVKVN	437
Db	200	KAVDWSGIVTAYTLLCGYPFPYDENDS-KLFEQQLKAEYEFDSYWDSDSADKDFIRN	258
Qy	438	LLVVDPEQRLTTKQALEHPMLQDDSMKHTVERLXMGVDHTMPPIKKNITRKRGHBDQ-	496
Db	259	LMKDPKPNKRYTCQAAHPIADTDLNKNTH-----ESVSAQRKNAFKSK-----WRQA	308
Qy	497	-----DASTSSCSELLPTSAEK	513
Db	309	FNATAVVRHMRKLUHGSLSLSSNAVSSSSLASOK	344
RESULT 14			
US-10-446-175-4			
; Sequence 4, Application US/10446175			
; Publication No. US2004001412A1			
; GENERAL INFORMATION:			
; APPLICANT: Donoho, Greg			
; APPLICANT: Turner, C. Alexander Jr.			

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-936-445-4

Query Match 22.2%; Score 603; DB 17; Length 356;
Best Local Similarity 38.1%; P-reqd. No. 1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;
Qy 198 IGGACGEVKLAQKSVCKVAVKILSKRKPEKMTSSNEHPISDVTEIEILKKLDHPCII 257
Db 29 LCTGAAFEVLAABEKATGKLFAVKCPKKALKGKES----SIENEIAVLRKGHENTV 82
Qy 258 KLENFFDSEDFYIVILEMGESELFDRVVNSTRLEPIAKLTYFYQMLLAQYLHENGVH 317
Db 83 ALEDIVESPNTLHYLMOLVSGELFDRIVEKGFYTEKDASLTLRQVLDAYAYLHRMGIVH 142
Qy 318 RDLKPENVLSSSTSECCIIKTDGQSKILGETSLMRTLCGCTPTYLAPEVLTAGTTGYS 377
Db 143 RDLKPENVLSSYSDQDEBSKIMISDFGUSRMEKGKDVNSTACSTPGVAPEVLI--AQKPY 199
Qy 378 SAVDCWSIGVILFVCLCGYPPESEQNNSNIPLNQIAEGKTYIAAAWRNTYSEQAFDLVQN 437
Db 200 KAVDCWSIGVAYILGCGPPYDENDS-KLFEQILKAEBFDSPPWDDDSAKDFIRN 258
Qy 438 LLVVDPSQRLLTKQALEHPILODDSMKHTVERLMLGVDHMPPIKKNNIRKRGHEWDO- 496
Db 259 LMEKDPNKRKTYCEQAARHPIWADTAANKNIIH-----ESVSAQIRKNEAKSK--WRQA 308
Qy 497 -----DASTSSCSEILPTEAK 513
Db 309 FNATAVVRHMRKLHGLSSNASVSSSLASQK 344

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Search completed: July 7, 2005, 13:06:39
 Job time : 165 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:50:39 ; Search time 43 Seconds
(without alignments)

897.525 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESSQQSQCTSSSS.....ASTSSCSELPTSAEKRKR 517

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
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2: /cgn2_6/ptodata/1/iaa/5B_COMBO:dep:
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6: /cgn2_6/ptodata/1/iaa/backfile1.dep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2712	100.0	517	4	US-09-849-617-2
2	1655.5	61.0	543	4	US-09-529-093A-2
3	1655.5	61.0	543	4	US-09-522-154-2
4	1589.5	58.6	490	4	US-09-949-016-10788
5	603	22.2	356	4	US-09-733-388-4
6	603	22.2	356	4	US-10-446-175-4
7	600.5	22.1	355	4	US-09-579-664B-10
8	600.5	22.1	355	4	US-10-355-975A-10
9	600.5	22.1	385	4	US-09-733-388-2
10	600.5	22.1	385	4	US-10-446-175-2
11	591.5	21.8	370	2	US-08-878-989-19
12	591.5	21.8	370	3	US-09-277-796-17
13	591.5	21.8	370	3	US-09-457-040B-31
14	591.5	21.8	370	4	US-09-538-092-1314
15	591.5	21.8	415	4	US-09-949-016-7461
16	591.5	21.8	415	4	US-09-949-016-7462
17	580.5	21.4	476	4	US-09-960-643-2
18	575.5	21.2	776	2	US-08-198-446B-17
19	575.5	21.2	821	1	US-08-870-693-17
20	575.5	21.2	821	1	US-08-198-446B-6
21	575.5	21.2	821	2	US-08-870-693-6
22	559.5	20.6	513	4	US-09-248-796A-18515
23	531	19.6	473	4	US-09-538-092-1353
24	525.5	19.4	358	4	US-09-896C-29
25	525.5	19.4	456	1	US-08-463-164-2
26	525.5	19.4	456	2	US-08-338-057-2
27	525.5	19.4	456	2	US-08-668-416-2

ALIGNMENTS

RESULT 1
US-09-849-617-2
; Sequence 2, Application US/09849617
; Patent No. 6593110
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: GUO, Zijian
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
; FILE REFERENCE: CIT1350-1
; CURRENT APPLICATION NUMBER: US/09/849,617
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/202,028
; SEQ ID NO: 14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-849-617-2

Query Match 100.0%; Score 2712; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 2e-254;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSRDTKTESSQQSQCTSSSS.....ASTSSCSELPTSAEKRKR 517
Db 1 MMSRDTKTESSQQSQCTSSSS.....ASTSSCSELPTSAEKRKR 517

Qy 1 MMSRDTKTESSQQSQCTSSSS.....ASTSSCSELPTSAEKRKR 517
Db 1 MMSRDTKTESSQQSQCTSSSS.....ASTSSCSELPTSAEKRKR 517

Qy 61 I PQPWGRWLWALKGKFNLHDCLHEEYFGDRKXCDTYDIPVQNTOTRYKTYSKHRIHQ 120
Db 61 I PQPWGRWLWALKGKFNLHDCLHEEYFGDRKXCDTYDIPVQNTOTRYKTYSKHRIHQ 120

Qy 61 I PQPWGRWLWALKGKFNLHDCLHEEYFGDRKXCDTYDIPVQNTOTRYKTYSKHRIHQ 120
Db 61 I PQPWGRWLWALKGKFNLHDCLHEEYFGDRKXCDTYDIPVQNTOTRYKTYSKHRIHQ 120

Qy 121 E LIGHGHERRVANTEEDLSQNGTFNKKEITIGKRTLPLTNNAEALSPLPNKVFSDSVDD 180
Db 121 E LIGHGHERRVANTEEDLSQNGTFNKKEITIGKRTLPLTNNAEALSPLPNKVFSDSVDD 180

Qy 181 QTYPKDFIDKYIMSPIGSAGCEYKLAFOKSVCCKVAKLISKPKFKMNTSSNBPHTS 240
Db 181 QTYPKDFIDKYIMSPIGSAGCEYKLAFOKSVCCKVAKLISKPKFKMNTSSNBPHTS 240

Qy 241 VDTIEILKKLDDHPCIKIENFFSDFFYVLEMEGGELFDRVNSTRLREPIAKLYF 300
Db 241 VDTIEILKKLDDHPCIKIENFFSDFFYVLEMEGGELFDRVNSTRLREPIAKLYF 300

Qy 241 VDTIEILKKLDDHPCIKIENFFSDFFYVLEMEGGELFDRVNSTRLREPIAKLYF 300
Db 241 VDTIEILKKLDDHPCIKIENFFSDFFYVLEMEGGELFDRVNSTRLREPIAKLYF 300

Qy 301 YMLLAVQYLHENGVIRHDLKPEPVNLISSTSBECCKITDQFQSKLIGETSLMRTLGTP 360
Db 301 YMLLAVQYLHENGVIRHDLKPEPVNLISSTSBECCKITDQFQSKLIGETSLMRTLGTP 360

Qy 301 YMLLAVQYLHENGVIRHDLKPEPVNLISSTSBECCKITDQFQSKLIGETSLMRTLGTP 360
Db 301 YMLLAVQYLHENGVIRHDLKPEPVNLISSTSBECCKITDQFQSKLIGETSLMRTLGTP 360

Qy 361 TYLAPEVINTAGTCYSSAVDCWSIGVILFVCLCGYPPSEONSNIPLKNOIAEGKTYI 420
 Db 361 TYLAPEVINTAGTCYSSAVDCWSIGVILFVCLCGYPPSEONSNIPLKNOIAEGKTYI 420
 Qy 421 AAARWVNSE QAFPLVNLVWDPERQLTQKALEHPWLQDSSMKTVERLMLGVDTMPP 480
 Db 421 AAARWVNSE QAFPLVNLVWDPERQLTQKALEHPWLQDSSMKTVERLMLGVDTMPP 480
 Qy 481 PIKKNIIRKGHEWDODASTSSCSELPTSAEKRKR 517
 Db 481 PIKKNIIRKGHEWDODASTSSCSELPTSAEKRKR 517

RESULT 3
 US-09-529-154-2
 ; Sequence 2, Application US/09529154
 ; GENERAL INFORMATION:
 ; APPLICANT: LUYTEN, Walter H.M.L.
 ; APPLICANT: PARKER, Andrew E.
 ; APPLICANT: MCGOWAN, Clare H.
 ; APPLICANT: BLASTINA, Alessandra
 ; TITLE OF INVENTION: Human Checkpoint Kinase, hcDSL, Compositions and Methods
 ; FILE REFERENCE: T3R1:64.9.0
 ; CURRENT APPLICATION NUMBER: US/09/529.093A
 ; PRIORITY APPLICATION NUMBER: PCT/EP98/06982
 ; CURRENT FILING DATE: 2000-04-07
 ; PRIORITY FILING DATE: 1998-10-21
 ; PRIORITY APPLICATION NUMBER: GB 9722320.0
 ; NUMBER OF SEQ ID NOS: 6
 ; SEQ ID NO 2
 ; LENGTH: 543
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-154-2

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
 Best Local Similarity 59.9%; Pred. No. 9e-152; Indels 39; Gaps 7;
 Matches 326; Conservative 74; Mismatches 105; InDelS 39; Gaps 7;

Qy 2 MSRDTKTESO-----
 Db 1 MSRESDVEAQSHGSSACSPHGSVTSQSSSSQGSSSQTGL 60

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
 Best Local Similarity 59.9%; Pred. No. 9e-152; Indels 39; Gaps 7;
 Matches 326; Conservative 74; Mismatches 105; InDelS 39; Gaps 7;

Qy 2 MSRDTKTESQ-----
 Db 1 MSRESDVEAQSHGSSACSPHGSVTSQSSSSQGSSSQTGL 60

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
 Best Local Similarity 59.9%; Pred. No. 9e-152; Indels 39; Gaps 7;
 Matches 326; Conservative 74; Mismatches 105; InDelS 39; Gaps 7;

Qy 38 SSLLDTPVQDLSI-----
 Db 61 SSLLTVSTQELYSPEQDPEQPEPAPWRLWALQDGFALEVNNDYWGKDKS 120

Qy 93 CDYTFDIPVNLQTDYKTSKRHRFRIFQELGHGHSRVANIEDLSGNGTFYNEKEIGKRT 152
 Db 121 CEYCFDEPLKRTDKYRYSKHFRIFREVGPKNSTAYIEDHSNGTFNTELYGKGR 180

Qy 153 LPITNNAEIALSLPTNKVFWFSDLSDQTYPKDFIDKIMMSRPIGSACGEVKAFOK 212
 Db 181 RPNNNSSIALSSRNKVFVFDLTDQSYPKALRDEYNSKTKGACGEVKAFOK 240

Qy 213 SVCKKVAVKIISKRKFMMNTSSNEHP- ISVDTETEILKLDHPCTIKIENPFDSEDFYYI 271
 Db 241 KTCKKVAVKIISKRKFMMNTSSNEHP- ISVDTETEILKLDHPCTIKIENPFDSEDFYYI 299

Qy 272 VLELMEGGELFDRVNSTRLEPIAKLYFYQMLLAQYLHENGIIHRDLKENVLLSSTS 331
 Db 300 VLELMEGGELFDRVNSTRLEPIAKLYFYQMLLAQYLHENGIIHRDLKENVLLSSTS 359

Qy 332 EECCKITDFGSKILGETSMRLTGTPTYLAPAEVLNTAGTTGYSAVDCWSIGVLFY 391
 Db 360 EDCLIKITDFGSKILGETSMRLTGTPTYLAPAEVLNTAGTTGYSAVDCWSIGVLFY 419

Qy 392 CLCGYPPFSEONSNIPLKNQIAEGKTYIAAWRNVSEQAFDLYKNNLWVDPERQLTTKQ 451
 Db 420 CLSGYPPFSEHRTQVSLKDQITSGKNTFPEVWAESEKALDLYKNNLWVDPKARFTTEE 479

Qy 452 ALEHPWLQDSSMKTVERLMLGVDTMPP--IKKNIIRKGHEWDODASTSS---C 503
 Db 480 ALRHPWLQDDEMKRKFQDLISEEESTALPQVLAQPSTSRKPRGEAEGAEETTRPAVC 539

Qy 504 SEIL 507 US-09-733-388-4 ; Sequence 4, Application US/09733388
 Db 540 AAVL 543 ; Patent No. 662698

RESULT 4
 US-09-949-016-10788 ; Sequence 10788, Application US/09949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949.016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 10788
 ; LENGTH: 490
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-10788

Query Match 58.6%; Score 1589.5; DB 4; Length 490;
 Best Local Similarity 64.0%; Pred. No. 2e-145; Indels 31; Gaps 5;
 Matches 310; Conservative 60; Mismatches 83;

Qy 2 MSRDTKESQ----- QSYSSSSSSAP-QSYSSSSGGT 37
 Db 1 MRSRDSVEAQSHGSSACSQPHGSVTSQGSQSSQSSQTSSTMNSQSSHSSGTL 60
 Qy 38 SSSLDTVPQDLSI-----PEDEDEIDEPQPGRLWALGKRFNHLQHCLHEPVYFGRDK 92
 Db 61 SSELFTVSTQDLSI-----SPEDEOPEPAPWALQDFANLCEVNNDYWFGRDK 120
 Qy 93 CDYTFDIPVQLNQTDYKTYSKRHRFRIFQELGHGHSRVAIEQLSGLNTFVNKEIIGKGR 152
 Db 121 CETCFDEPPLRDRDKYRISKGHRFIREVGPNSTIAYIEDHSGNFTVNTELVGGR 180
 Qy 153 LPLTNNABIALSULPTNKFVFSPLSVDQDTIYPKDFIDKYIMSRPITGSGACEGVKLAFOK 212
 Db 181 RPLANNNSPLLSRSRNKFVFFDLTVDDQSYVPKALRDEYIMTSKLGSGACEGVKLAFAER 240
 Qy 213 SVCKVAVKIIISRKFRNTTSSEHP-TSVDTEIELLKRLDPCTIKIENFDSEDFYI 271
 Db 241 KTKCKVAVKIIISRKFAAGGSAEADPAINVETEILKLLNPKTICKNFEADE-YYI 299

Query Match 22.2%; Score 603; DB 4; Length 356;
 Best Local Similarity 38.1%; Pred. No. 7e-20; Indels 40; Gaps 6;
 Matches 128; Conservative 62; Mismatches 106;

Qy 198 IGGAGCSEBVKLAFOKSVCKVAVKIIISRKFRNTTSNEHPLSVDDPBLKLDLDPCTI 257
 Db 29 LGTGAFFSEVVLVALEEKATGKLFAVKCPKPKALKGKES-----SIEBIAVLRKIGHENIV 82

Query Match 22.2%; Score 603; DB 4; Length 356;
 Best Local Similarity 38.1%; Pred. No. 7e-20; Indels 40; Gaps 6;
 Matches 128; Conservative 62; Mismatches 106;

Qy 258 KLENFDFSEDFYYIVLMEGGELFDRVNVNSTRLEPIAKLYFYQMLAYOYLHENGVH 317
 Db 83 ALEDIVIESPNHLYLVNQLVSGELPPIVEKGFTYEDASTLIRQLDYLHMGIVH 142

Qy 318 RDLKPENVLSSSTSBECCIKITDFGGSKILGETSLMRLCGTPYLAPEVLTAGTGYS 377
 Db 143 RDLKPENPLLYSQDEBSKIMISDFGLSKMECGDYNISTACCTPGYAPEVLI--AQKPY5 199

Qy 378 SAVDCSLGVILFVCGYPPFSEQNSNIPKLNQALAEKTYIAAMWRNVSIEQAFLVKN 437
 Db 200 KAVDCNSIGVIAYLQGPPFYDENDS-KLFEQILKAEYEDSPWDDISDSAKFIRN 258

Qy 438 LLVVDPEQRLLTQKALBHPWLQDDSNKHTYVERLMTGVDHTMPPPKQNLIRKGHENDO- 496
 Db 259 LMEKDPNKRYTCEQARHPWADTAIKNH-----ESVSAQ1RKNPFAKSK--WRQA 308

Qy 497 ----- DASTSSCSEI^LPTSAEK 513
 Db 309 ENATAVYVHMRKLHJGSSLDSNASTVSSSLASQK 344

RESULT 6
 US-10-446-175-4 ; Sequence 4, Application US/10446175
 ; Patent No. 6806073
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Greg
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambowicz, Brian
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Sandra, Arthur T.
 ; TITLE OF INVENTION: No. 6806073 Human Kinase Proteins and Polynucleotides Encoding the Same
 ; FILE REFERENCE: IEX-010-3-USA
 ; CURRENT APPLICATION NUMBER: US/10/446,175
 ; CURRENT FILING DATE: 2003-05-27
 ; PRIOR APPLICATION NUMBER: US/09/733,388

Qy 452 ALRH 455
 Db 480 ALRH 483

RESULT 5

PRIOR FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,428
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-446-175-4

Query Match 22.2%; Score 603; DB 4; Length 356;
 Best Local Similarity 38.4%; Pred. No. 7.7e-50;
 Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

Db 19 IGGGACCBVKLAQKSVCKAVKIKTSKRKFKMTTSNEHPIVSUTEIELKKLDHPGII 257
 Db 29 LGGTGAEEVVAEEKATGKLPKAKLGKES----SIENIAVLRKIRHENIV 82

RESULT 8

Qy 258 KIENFPDSEDFYYVIBLMEGGELFDRVNSTRLEPAKLYFYQMLLAQYIHLHENGVIH 317
 Db 83 ALEDIVESPNNHLYNQVSGELFDRIVEKGFTYKDASTLIRQDAVYLHMRGIVH 142

Qy 318 RDLKPENVLJSSTSEECIIKTDGOSKILGETSLMRTLCGPTVLAPEVLTAGTTGYS 377
 Db 143 RDLKPENVLJSQDEESKIMISDFGHSKMEKGDMSTACGTPGTVAPEVLI--AQKPY 199

Qy 378 SAVDCMSLGVILFVCLCGYPPEQSNSNIPKLNQIAEGKTYIAAAWRNVSSEQADLVN 437
 Db 200 KAVDCMSLGVATYIILCGYPPEFYDENDS-KLFEQIKAEEFDSPYWDISDAKDFIRN 258

Qy 438 LLVVDPEQRLTTKQALEHPLWQDLSMKHTVERLMLYGVDHMPPPIKKLNIRKRGHEDQ- 496
 Db 259 LMEKDPNKRVTCEQAHRHPTAGDT----ALSNIHESVSAQIRKNPFSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVVRHMRRQLQGSSLDSSNAVSSNLSASQK 345

Query Match 22.1%; Score 600.5; DB 4; Length 355;
 Best Local Similarity 38.4%; Pred. No. 1.3e-49;
 Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

Db 19 IGGGACCBVKLAQKSVCKAVKIKTSKRKFKMTTSNEHPIVSUTEIELKKLDHPGII 257
 Db 29 LGGTGAEEVVAEEKATGKLPKAKLGKES----SIENIAVLRKIRHENIV 82

RESULT 9

Qy 438 LLVVDPEQRLTTKQALEHPLWQDLSMKHTVERLMLYGVDHMPPPIKKLNIRKRGHEDQ- 496
 Db 259 LMEKDPNKRVTCEQAHRHPTAGDT----ALSNIHESVSAQIRKNPFSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVVRHMRRQLQGSSLDSSNAVSSNLSASQK 345

Query Match 22.1%; Score 600.5; DB 4; Length 355;
 Best Local Similarity 38.4%; Pred. No. 1.3e-49;
 Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

Db 19 IGGGACCBVKLAQKSVCKAVKIKTSKRKFKMTTSNEHPIVSUTEIELKKLDHPGII 257
 Db 29 LGGTGAEEVVAEEKATGKLPKAKLGKES----SIENIAVLRKIRHENIV 82

Qy 258 KIENFPDSEDFYYVIBLMEGGELFDRVNSTRLEPAKLYFYQMLLAQYIHLHENGVIH 317
 Db 83 ALEDIVESPNNHLYNQVSGELFDRIVEKGFTYKDASTLIRQDAVYLHMRGIVH 142

Qy 318 RDLKPENVLJSSTSEECIIKTDGOSKILGETSLMRTLCGPTVLAPEVLTAGTTGYS 377
 Db 143 RDLKPENVLJSQDEESKIMISDFGHSKMEKGDMSTACGTPGTVAPEVLI--AQKPY 199

Qy 378 SAVDCMSLGVILFVCLCGYPPEQSNSNIPKLNQIAEGKTYIAAAWRNVSSEQADLVN 437
 Db 200 KAVDCMSLGVATYIILCGYPPEFYDENDS-KLFEQIKAEEFDSPYWDISDAKDFIRN 258

Qy 438 LLVVDPEQRLTTKQALEHPLWQDLSMKHTVERLMLYGVDHMPPPIKKLNIRKRGHEDQ- 496
 Db 259 LMEKDPNKRVTCEQAHRHPTAGDT----ALSNIHESVSAQIRKNPFSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVVRHMRRQLQGSSLDSSNAVSSNLSASQK 345

Query Match 22.1%; Score 600.5; DB 4; Length 355;
 Best Local Similarity 38.4%; Pred. No. 1.3e-49;
 Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

Db 19 IGGGACCBVKLAQKSVCKAVKIKTSKRKFKMTTSNEHPIVSUTEIELKKLDHPGII 257
 Db 29 LGGTGAEEVVAEEKATGKLPKAKLGKES----SIENIAVLRKIRHENIV 82

Qy 258 KIENFPDSEDFYYVIBLMEGGELFDRVNSTRLEPAKLYFYQMLLAQYIHLHENGVIH 317
 Db 83 ALEDIVESPNNHLYNQVSGELFDRIVEKGFTYKDASTLIRQDAVYLHMRGIVH 142

GENERAL INFORMATION:

APPLICANT: Donoho, Greg
 APPLICANT: Scoville, John
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Friedrich, Glenn
 APPLICANT: Zambrowicz, Brian
 APPLICANT: Abuin, Alejandro
 APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0103-USA

CURRENT APPLICATION NUMBER: US/09/733,388

PRIOR APPLICATION NUMBER: 2000-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 5

SEQUENCE ID NO: 2

TYPE: PRT

ORGANISM: Homo sapiens

US-09-733-388-2

Query Match 22.1%; Score 600.5; DB 4; Length 385;

Best Local Similarity 38.4%; Pred. No. 1.5e-19; Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

Qy 198 IGGAGCEVKLAFQSKVCKVAVKLTISKRFKNTSSNEHPISVDTIEILKLDIFCII 257
 Db 29 LGTGAFFSEVVALEAKTGKLFAVKCPKKALKGKES---SIEBEAVLRKIKHENIV 82

Qy 258 KIENFFDSEDFYIVLBMEGGELFDPRVNSTRLEPIAKLYFYOMLLAVOYLHENGVIH 317
 Db 83 ALEDIYESPNNLYLQVSGELFDIVERGFTYKTDASTLIRQVTLHNGIVH 142

Qy 318 RDLKPENVLLSSTSBECCIKITDEGSKILGETSLMRLCGPTVLAPEVLNTAGTGYS 377
 Db 143 RDLKPENLILYQDDESKIMISDFGLSKMKGDIWSTACCTPGVYAPEVL--AQKPY 199

Qy 378 SAVDCWSLGVLFCVQGYPPEQNSNIPKNOIAEGKTYIAAWRNSVSEQAFLVKN 437
 Db 200 KAVDCWSLGVIAYILCGYPFYDENDS-KLFEQIILKAEEFDSPWDDSDSAKDFIRN 258

Qy 438 LLVVDPDEORLITTKOALEHPWLTQDDSMKHTVERLMLGYDHTMPPPIKKNIIRKRGHEDQ- 496
 Db 259 LMEDKDPNKRRTYCEQAARHPWAGDT---ALRNKIHESVSAQIRKNFARKSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVYRHRMRKLHLGSSLDSNSASTSSSLASQK 345

RESULT 11

US-08-878-989-19

Qy 378 SAVDCWSLGVLFCVQGYPPEQNSNIPKNOIAEGKTYIAAWRNSVSEQAFLVKN 437
 Db 200 KAVDCWSLGVIAYILCGYPFYDENDS-KLFEQIILKAEEFDSPWDDSDSAKDFIRN 258

Qy 438 LLVVDPDEORLITTKOALEHPWLTQDDSMKHTVERLMLGYDHTMPPPIKKNIIRKRGHEDQ- 496
 Db 259 LMEDKDPNKRRTYCEQAARHPWAGDT---ALRNKIHESVSAQIRKNFARKSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVYRHRMRKLHLGSSLDSNSASTSSSLASQK 345

RESULT 10

US-10-446-175-2

Sequence 2, Application US/10446175

Patent No. 6806073

GENERAL INFORMATION:

APPLICANT: Donoho, Greg
 APPLICANT: Scoville, John
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Friedrich, Glenn
 APPLICANT: Zambrowicz, Brian
 APPLICANT: Abuin, Alejandro
 APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0103-USA

CURRENT APPLICATION NUMBER: US/09/733,388

PRIOR FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,428

PRIOR FILING DATE: 1999-12-07

GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 385

TYPE: PRT

ORGANISM: Homo sapiens

US-10-446-175-2

Query Match 22.1%; Score 600.5; DB 4; Length 385;

Best Local Similarity 38.4%; Pred. No. 1.5e-19; Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

Qy 198 IGGAGCEVKLAFQSKVCKVAVKLTISKRFKNTSSNEHPISVDTIEILKLDIFCII 257
 Db 29 LGTGAFFSEVVALEAKTGKLFAVKCPKKALKGKES---SIEBEAVLRKIKHENIV 82

Qy 258 KIENFFDSEDFYIVLBMEGGELFDPRVNSTRLEPIAKLYFYOMLLAVOYLHENGVIH 317
 Db 83 ALEDIYESPNNLYLQVSGELFDIVERGFTYKTDASTLIRQVTLHNGIVH 142

Qy 318 RDLKPENVLLSSTSBECCIKITDEGSKILGETSLMRLCGPTVLAPEVLNTAGTGYS 377
 Db 143 RDLKPENLILYQDDESKIMISDFGLSKMKGDIWSTACCTPGVYAPEVL--AQKPY 199

Qy 378 SAVDCWSLGVLFCVQGYPPEQNSNIPKNOIAEGKTYIAAWRNSVSEQAFLVKN 437
 Db 200 KAVDCWSLGVIAYILCGYPFYDENDS-KLFEQIILKAEEFDSPWDDSDSAKDFIRN 258

Qy 438 LLVVDPDEORLITTKOALEHPWLTQDDSMKHTVERLMLGYDHTMPPPIKKNIIRKRGHEDQ- 496
 Db 259 LMEDKDPNKRRTYCEQAARHPWAGDT---ALRNKIHESVSAQIRKNFARKSK--WRQA 309

Qy 497 -----DASTSSCSEILPTSAEK 513
 Db 310 FNATAVYRHRMRKLHLGSSLDSNSASTSSSLASQK 345

RESULT 11

US-08-878-989-19

Sequence 19, Application US/08878989

Patent No. 5885803

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guglieri, Karl G.
 APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISPARSE ASSOCIATED PROTEIN
 TITLE OF INVENTION: KINESSES
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,989
 FILING DATE:
 CLASIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J J

REGISTRATION NUMBER: 36,749
 TELECOMMUNICATION DOCKET NUMBER: PF-0321 US
 TELEPHONE: 415-855-0555
 TELEX: 415-845-4166

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 370 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 790790

US-08-878-989-19

Query Match Similarity 21.8%; Score 591.5; DB 2; Length 370;
 Best Local Similarity 39.9%; Pred. No. 1.1e-48;
 Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

Qy 186 KDFIDKYMRSPIGSAGCIVKLAQKSVCKVAVKIIISRKFKRNTSSNEHPIVDTEI 245
 Db 14 EDIRDYDFRDVLGTFSEVLAEDKRTQKVAVKCIAREGKSMEN-----EI 67
 Qy 246 EILKLDHPCLIKIENPFDSEDFYYIVLMEGLDFDRVNSTRLEPAAKLYFYQMLL 305
 Db 68 AVLHKIKHPNIVVALDIYESEGGHLYLIMQLYSGGELFDRIVEKGFYTERASRLIQVLD 127
 Qy 306 AVQYLHENGVTHRDLPENVLLSSTSSEBCCIKITDFGQSKILGETSLMRTLCGPTTYLAP 365
 Qy 128 AVKYLHDLGIVERDLKPENLILYSSLOEDSKTMISDFGLSMEDPESVLSAACGTPGYVAP 187
 Db 188 EVLNNTAGTGTGSSAVDCWSLGYLFLFCVLCGPPFSEONSNIPLNQIAEGSKYTIAAANR 425
 Db 188 EVL---AQKEYSKAVDCWSIGVAYILLCGPPFYDEN--DAKLFEQILKAEYEFDSPYND 243
 Qy 426 NVSEQAEDLVKNNLUVDPERQILTTKALEHFLQDDSMRHTKVERUMLGVHRTMPPPIKNN 485
 Db 244 DISDSAKDFIRHLMERDPEKRFCTCEQALQHMIAGDT-----ALDKNTHQSVEQIKNN 297
 Qy 486 IIRKGHEDQ 496
 Db 298 FAKSK---WKQ 305

RESULT 12
 US-09-272-796-19
 Sequence 19, Application US/09272796
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/272-796
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/878, 989
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J. J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0321 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 370 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 790790

US-09-272-796-19

Query Match Similarity 21.8%; Score 591.5; DB 3; Length 370;
 Best Local Similarity 39.9%; Pred. No. 1.1e-48;
 Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

Qy 186 KDFIDKYMRSPIGSAGCIVKLAQKSVCKVAVKIIISRKFKRNTSSNEHPIVDTEI 245
 Db 14 EDIRDYDFRDVLGTFSEVLAEDKRTQKVAVKCIAREGKSMEN-----EI 67
 Qy 246 EVLNNTAGTGTGSSAVDCWSLGYLFLFCVLCGPPFSEONSNIPLNQIAEGSKYTIAAANR 425
 Db 188 EVL---AQKEYSKAVDCWSIGVAYILLCGPPFYDEN--DAKLFEQILKAEYEFDSPYND 243
 Qy 426 NVSEQAEDLVKNNLUVDPERQILTTKALEHFLQDDSMRHTKVERUMLGVHRTMPPPIKNN 485
 Db 244 DISDSAKDFIRHLMERDPEKRFCTCEQALQHMIAGDT-----ALDKNTHQSVEQIKNN 297
 Qy 486 IIRKGHEDQ 496
 Db 298 FAKSK---WKQ 305

RESULT 13
 US-09-457-040B-31
 Sequence 31, Application US/09457040B
 ; GENERAL INFORMATION:
 ; APPLICANT: Vertex Pharmaceuticals Incorporated
 ; TITLE OF INVENTION: Crystallized P38 Complexes
 ; FILE REFERENCE: VPI 98-14
 ; PATENT NO. 6387611
 ; CURRENT APPLICATION NUMBER: US/09/457, 040B
 ; CURRENT FILING DATE: 1999-12-08
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-457-040B-31

Query Match Similarity 21.8%; Score 591.5; DB 3; Length 370;
 Best Local Similarity 39.9%; Pred. No. 1..1e-48;
 Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

Qy 186 KDFIDKYMSPRGSGACCEVKLAFOKSCKRKVAKVLTISRKPKMTNTSSNEHPISYDTEI 245
 Db 14 EDIRDIVDRDVGTLGAFSEVILAEDETRQLVAKCTAKEALEGEGSMEN-----EI 67

Qy 246 EILKKLDHPCIIKENFFPDSDFYYIVLELMEGELFDRVNISTRLEPIAKLYFYQMLI 305
 Db 68 AVLHKIKHENIVALDLYIYESGGHLYLIMQLVSGELFDRIVEKGFTTERDASRLIQVLD 127

Qy 306 AVOYLHENGVIHDLKPKENVLSLSSTSECCIKITDFGSKLGETSLMRTLCGTPYIAP 365
 Db 128 AVKYLHDIGI VHDLKPKENLYLSDLEPSKIMISDFGJSKRMDDPGSVLSTACGTPGVAP 187

Qy 366 EVLNLTAGTTGYSASSAVDCNSLGSVLFVCLCGYPFSEQNSNIPPLKNQIAEGKTYIAAWR 425
 Db 188 EVL---AQKPYSKAVDCMISGIVTAYLICGYPFYDEN-DAKLFEQIKAEEYEDPSYMD 243

Qy 426 NVSQAOFDVKNLLVVDPEQRLLTQAKLWQDDSMKHTVERLMLGVDTMPPEPPIKNN 485
 Db 244 DISDSAOFDRLGAFSEVILAEDETRQLVAKCTAKEALEGEGSMEN-----EI 297

Qy 486 IIRKGHEDWQ 496
 Db 298 FAKSK---WKQ 305

RESULT 15
 US-09-949-016-7461
 ; Sequence 7461, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,766
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 7461
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-7461

Query Match 21.8%; Score 591.5; DB 4; Length 415;
 Best Local Similarity 39.9%; Pred. No. 1..1e-48;
 Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

Qy 186 KDFIDKYMSPRGSGACCEVKLAFOKSCKRKVAVLISRKPKMTNTSSNEHPISYDTEI 245
 Db 59 EDIRDIVDRDVGTLGAFSEVILAEDETRQLVAKCTAKEALEGEGSMEN-----EI 112

Qy 246 EILKKLDHPCIIKENFFPDSDFYYIVLELMEGELFDRVNISTRLEPIAKLYFYQMLI 305
 Db 113 AVLHKIKHENIVALDLYIYESGGHLYLIMQLVSGELFDRIVEKGFTTERDASRLIQVLD 172

Qy 306 AVOYLHENGVIHDLKPKENVLSLSSTSECCIKITDFGSKLGETSLMRTLCGTPYIAP 365
 Db 173 AVKYLHDIGI VHDLKPKENLYLSDLEPSKIMISDFGJSKRMDDPGSVLSTACGTPGVAP 232

Qy 366 EVLNLTAGTTGYSASSAVDCNSLGSVLFVCLCGYPFSEQNSNIPPLKNQIAEGKTYIAAWR 425
 Db 233 EVL---AQKPYSKAVDCMISGIVTAYLICGYPFYDEN-DAKLFEQIKAEEYEDPSYMD 288

Qy 426 NVSQAOFDVKNLLVVDPEQRLLTQAKLWQDDSMKHTVERLMLGVDTMPPEPPIKNN 485
 Db 289 DISDSAOFDRLGAFSEVILAEDETRQLVAKCTAKEALEGEGSMEN-----EI 342

Qy 486 IIRKGHEDWQ 496
 Db 343 FAKSK---WKQ 350

Query Match 21.8%; Score 591.5; DB 4; Length 370;
 Best Local Similarity 39.9%; Pred. No. 1..1e-48;
 Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

Qy 186 KDFIDKYMSPRGSGACCEVKLAFOKSCKRKVAVLISRKPKMTNTSSNEHPISYDTEI 245
 Db 14 EDIRDIVDRDVGTLGAFSEVILAEDETRQLVAKCTAKEALEGEGSMEN-----EI 67

Qy 246 EILKKLDHPCIIKENFFPDSDFYYIVLELMEGELFDRVNISTRLEPIAKLYFYQMLI 305
 Db 68 AVLHKIKHENIVALDLYIYESGGHLYLIMQLVSGELFDRIVEKGFTTERDASRLIQVLD 127

Qy 306 AVOYLHENGVIHDLKPKENVLSLSSTSECCIKITDFGSKLGETSLMRTLCGTPYIAP 365
 Db 128 AVKYLHDIGI VHDLKPKENLYLSDLEPSKIMISDFGJSKRMDDPGSVLSTACGTPGVAP 187

Search completed: July 7, 2005, 13:03:49
 Job time : 44 sec

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